



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 155135

TO: Emily M Le
Location: 3c35/3c18
Art Unit: 1648
Friday, June 03, 2005

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Case Serial Number: 08/869386

Noble.jarrell@uspto.gov

Search Notes

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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CRFE 155183

Jarrell, Noble

From: Le, Emily
Sent: Wednesday, June 01, 2005 6:34 PM
To: Jarrell, Noble
Subject: FW: Sequence Search: 08869386

Hi Noble,

I noted a discrepancy in an amino acid residue present in SEQ ID NO: 3. Thus, please provide another search for seq id no:3 ,wherein the sequence is: NNTRKSIRIQRGPGRAFVTIGKIG.

Thanks, Noble!!

-----Original Message-----

From: Le, Emily
Sent: Monday, May 16, 2005 12:04 PM
To: Jarrell, Noble
Subject: FW: Sequence Search: 08869386

update:

Please provide a search for the following:

1. RAFVTIGK, which is SEQ ID NO: 5 in the above case.
2. SEQ ID NO: 1
3. SEQ ID NO: 3

Please also limit the size to no more than 25 amino acids.

Thanks, Noble.

Emily

-----Original Message-----

From: Le, Emily
Sent: Friday, May 13, 2005 4:13 PM
To: Jarrell, Noble
Subject: Sequence Search: 08869386

Noble,

Please provide a search for the following:

1. RAFVTIGK

Please also limit the size to no more than 25 amino acids.

Thanks!

Emily Le

Noble
Done 6/3/05
2 AFA
Compare 1/6
10 prep
10 cond

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 03:11:57 ; Search time 38 Seconds
(without alignments)
60.768 Million cell updates/sec

Title: SEQ1
Perfect score: 122.11111111111111
Sequence: 1 Mntfkrkltidrgpgrafvtgikg 24

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4989

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 250 summaries

Database : PIR 79:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	52.5	20	2	S65399
2	29	23.8	17	2	S66213
3	27	22.1	20	2	S48654
4	26.5	21.7	14	2	PA0109
5	26.5	21.7	14	2	PA0045
6	26	21.3	13	2	S03879
7	25	20.5	10	2	D28077
8	25	20.5	12	2	S11286
9	25	20.5	16	2	JN0284
10	24.5	20.1	17	2	A37823
11	24	19.7	7	2	PT0515
12	24	19.7	13	2	C53275
13	24	19.7	14	2	PH0915
14	24	19.7	20	2	S63490
15	24	19.7	21	2	S31427
16	24	19.7	22	2	C42856
17	24	19.7	24	2	S21511
18	24	19.7	25	2	D41575
19	23.5	19.3	22	2	A28524
20	23	18.9	10	2	S65388
21	23	18.9	15	2	PH0797
22	23	18.9	17	2	S15203
23	23	18.9	17	2	A20293
24	23	18.9	18	2	S39153
25	23	18.9	19	2	I49037
26	23	18.9	20	2	B53592
27	23	18.9	24	2	C47689
28	23	18.9	25	2	B47689
29	22	18.0	12	2	S65629

30	22	18.0	20	2	S03505	T-cell receptor al
31	22	18.0	20	2	S31220	B2k protein - bovi
32	22	18.0	20	2	B47642	T-cell surface gly
33	22	18.0	20	2	DIRT	dental fluid tra
34	22	18.0	21	2	A60225	pyruvate dehydrog
35	22	18.0	22	2	PQ0070	T-cell receptor be
36	22	18.0	22	2	B9096	probable transcrip
37	22	18.0	23	2	S47192	T-cell receptor J-
38	22	18.0	23	2	G69812	hypothetical prote
39	22	18.0	24	2	D27579	T-cell receptor be
40	22	18.0	25	1	ZJBPG4	gene J protein - p
41	22	18.0	25	2	S26273	glyceroldehyde-3-p
42	22	18.0	25	2	S22221	peroxidase (EC 1.1
43	22	18.0	25	2	S10850	alpha-amylase inhi
44	21	17.2	10	2	S77990	cytochrome-c oxida
45	21	17.2	13	2	S33800	chaperone, TCP1-re
46	21	17.2	14	2	PH1347	Ig heavy chain DJ
47	21	17.2	16	2	H41299	T-cell receptor al
48	21	17.2	16	2	A42411	myosin light chain
49	21	17.2	16	2	S15879	cystathionine beta
50	21	17.2	18	2	S09722	2S albumin small c
51	21	17.2	21	2	S50535	calmodulin - elect
52	21	17.2	22	2	A39269	LX-1 tumor antigen
53	21	17.2	23	2	S43765	ribosomal protein
54	21	17.2	24	4	T01780	probable gag polym
55	21	17.2	25	2	S51071	ribosomal protein
56	21	17.2	25	2	B69274	hypothetical prote
57	21	17.2	25	2	S65729	hemoglobin, extrac
58	20.5	16.8	18	2	A25941	Ig heavy chain J-H
59	20.5	16.8	24	2	D53402	glTX 5'-region con
60	20	16.4	9	4	I73804	hypothetical E2 pr
61	20	16.4	11	2	S13279	lie-Ser-bradykinin
62	20	16.4	15	2	S43634	cytochrome-c oxida
63	20	16.4	15	2	S57577	T-cell receptor V-
64	20	16.4	15	2	D28587	T-cell receptor be
65	20	16.4	15	2	C34874	transforming prote
66	20	16.4	16	2	PH1790	T cell receptor al
67	20	16.4	16	2	PH1771	T cell receptor al
68	20	16.4	16	2	C49048	T-cell receptor be
69	20	16.4	16	2	PH1580	Ig H chain V-D-J r
70	20	16.4	17	2	B61321	histone H4 - chick
71	20	16.4	17	2	A61321	histone H4 - commo
72	20	16.4	18	2	PQ0072	T-cell receptor be
73	20	16.4	18	2	S28396	T-complex protein
74	20	16.4	19	2	A33361	CAMP-regulated pho
75	20	16.4	20	1	LPB8TT	tet leader peptide
76	20	16.4	20	2	A36016	granulocyte inhibi
77	20	16.4	20	2	A61264	MHC class I histoc
78	20	16.4	20	2	S68620	histone H4 - sea u
79	20	16.4	20	2	S65884	translation initia
80	20	16.4	20	2	S16478	tray protein - Esc
81	20	16.4	20	2	PS0188	superoxide dismuta
82	20	16.4	20	2	A42865	Ca2+/calmodulin-de
83	20	16.4	20	2	A42267	J-kappa recombinat
84	20	16.4	21	2	S47202	T-cell receptor J-
85	20	16.4	22	2	S47206	T-cell receptor be
86	20	16.4	22	2	S05590	hypothetical 2.5K
87	20	16.4	22	2	JC1488	H4-transferring tw
88	20	16.4	22	2	PC7072	cytochrome-c oxida
89	20	16.4	23	2	S43289	histone H4-1 precu
90	20	16.4	23	2	S15431	mannose-1-phosphat
91	20	16.4	24	2	A47415	Ig kappa chain V-I
92	20	16.4	24	2	B30609	histone H4 - alfal
93	20	16.4	24	2	B43295	extracellular mura
94	20	16.4	24	2	A43941	fibronectin recept
95	20	16.4	24	2	A37825	cytochrome-c oxida
96	20	16.4	25	2	S43633	alanine racemase (
97	20	16.4	25	2	PC1221	heat shock protein
98	20	16.4	25	2	A60807	neuromedin U - com
99	20	16.4	25	2	A34179	insulin-like growt
100	20	16.4	25	2	A60741	Ig heavy chain V r
101	20	16.4	25	2	S63378	hydrogensulfite re
102	20	16.4	25	2	S21197	

103	20	16.4	25	2	A61457	alpha-glucosidase	176	19	15.6	24	2	B60422	MSBL-neurophysin -
104	19.5	16.0	15	2	F28587	T-cell receptor be	177	19	15.6	24	2	PH1916	T-cell receptor be
105	19.5	16.0	18	2	S03528	Ig heavy chain J1	178	19	15.6	24	2	A53591	envelope protein g
106	19.5	16.0	20	2	A47687	3-dehydroquininate d	179	19	15.6	24	2	UC4804	core protein J - p
107	19	15.6	7	2	A33098	244K exoantigen -	180	19	15.6	24	2	S22333	gene J protein - p
108	19	15.6	9	2	E41978	calliFMRamide 5 -	181	19	15.6	24	2	PC2176	exo-alpha-sialidas
109	19	15.6	9	2	B20569	serum amyloid P-co	182	19	15.6	24	2	PH1336	Ig heavy chain DJ
110	19	15.6	10	2	PH1345	Ig heavy chain DJ	183	19	15.6	24	2	T24611	hypothetical prote
111	19	15.6	11	2	C37196	bradykinin-potenti	184	19	15.6	25	2	S07574	malate dehydrogena
112	19	15.6	12	2	D37196	bradykinin-potenti	185	19	15.6	25	2	S12997	pancreatic endopep
113	19	15.6	12	2	D46662	collagen alpha 2(V	186	19	15.6	25	2	D26889	T-cell receptor be
114	19	15.6	12	2	D28551	hypothetical prote	187	19	15.6	25	2	F49533	T-cell receptor be
115	19	15.6	12	2	C20907	Ig kappa-1 chain J	188	19	15.6	25	2	PH1354	Ig heavy chain DJ
116	19	15.6	12	2	F20907	Ig kappa-2 chain J	189	18.5	15.2	23	2	B26091	leukocyte glycopro
117	19	15.6	13	2	S23640	Ig kappa chain J s	190	18.5	15.2	25	2	B37520	glutathione transf
118	19	15.6	13	2	I50173	alpha-2 collagen -	191	18	14.8	5	2	S53595	hypothetical prote
119	19	15.6	14	2	B61309	lutropin beta chai	192	18	14.8	9	2	S39437	D-amino-acid oxida
120	19	15.6	14	2	S11074	alcohol dehydrogen	193	18	14.8	9	2	B45020	probable minipolyp
121	19	15.6	15	2	PH1342	Ig heavy chain DJ	194	18	14.8	9	4	EC1Q1M	orf 2 rara 5'-regi
122	19	15.6	15	2	I53284	T-cell receptor be	195	18	14.8	10	1	S24190	tachykinin I - mig
123	19	15.6	15	2	I78838	flt3 ligand isofo	196	18	14.8	10	2	A27617	tryptase (BC 3.4.2
124	19	15.6	15	2	PT0091	H+-transporting tw	197	18	14.8	10	2	S28506	triose-phosphate i
125	19	15.6	15	2	A36279	chemoattractant pr	198	18	14.8	10	2	S33300	collagen alpha 1(V
126	19	15.6	15	2	S08301	epidermal growth f	199	18	14.8	11	2	A56878	probable substance
127	19	15.6	16	2	FT0224	Ig heavy chain CDR	200	18	14.8	12	2	PH0799	light yellow cell
128	19	15.6	16	2	G49039	T-cell receptor be	201	18	14.8	13	2	B61308	T-cell receptor al
129	19	15.6	16	2	B28587	T-cell receptor be	202	18	14.8	14	2	PH1332	Ig heavy chain DJ
130	19	15.6	16	2	F53284	T-cell receptor al	203	18	14.8	14	2	B28018	very late antigen-
131	19	15.6	16	2	PH1453	T-cell receptor al	204	18	14.8	14	2	PH0804	T-cell receptor al
132	19	15.6	16	2	E58501	25K kidney and gal	205	18	14.8	14	2	G61308	hemocyanin chain 3
133	19	15.6	16	2	I37452	protein kinase - h	206	18	14.8	14	2	S13973	hydrogensulfite re
134	19	15.6	16	2	S78415	ribosomal protein	207	18	14.8	15	2	PA0034	chlorophyll a/b-bi
135	19	15.6	16	2	A44897	ferredoxin-NADP re	208	18	14.8	15	2	PA0070	protein QA300024 -
136	19	15.6	16	4	A33171	hypothetical prote	209	18	14.8	15	2	A56970	GLYNA1 - soybean (
137	19	15.6	17	2	B49404	T-cell receptor be	210	18	14.8	15	2	PA0106	protein QF200076 -
138	19	15.6	17	2	D53284	T-cell receptor be	211	18	14.8	15	2	A56963	acid phosphatase (
139	19	15.6	17	2	S05033	photosystem II pro	212	18	14.8	15	2	A28497	neurotensin-relate
140	19	15.6	18	2	I73024	T cell receptor be	213	18	14.8	15	2	JT0610	leukocyte chemoatt
141	19	15.6	18	2	B40741	T-cell receptor be	214	18	14.8	15	2	A21425	cytochrome P450 IF
142	19	15.6	18	2	A61392	brain-associated s	215	18	14.8	16	2	B41425	fibronopeptide A -
143	19	15.6	18	2	PH1350	Ig heavy chain DJ	216	18	14.8	16	2	H29501	L-serine dehydrata
144	19	15.6	18	2	A49404	T-cell receptor be	217	18	14.8	16	2	S16376	caldesmon - turkey
145	19	15.6	18	2	S70612	alpha-macroglobuli	218	18	14.8	16	2	A35552	L-ascorbate peroxi
146	19	15.6	18	2	S60269	tubulin beta-3 cha	219	18	14.8	17	2	S32587	Ig heavy chain CRD
147	19	15.6	19	2	S22233	vitronectin - shee	220	18	14.8	17	2	PT0235	T-cell receptor be
148	19	15.6	20	1	LFBS7U	tet leader peptide	221	18	14.8	17	2	I24687	lactase-philorizin
149	19	15.6	20	2	S17461	flavodoxin B - Azo	222	18	14.8	17	2	A46592	hypothetical prote
150	19	15.6	20	2	S04961	malate dehydrogena	223	18	14.8	17	2	S61451	CD33 antigen homol
151	19	15.6	20	2	B60894	crystallin - Pacif	224	18	14.8	17	2	I67524	S locus-linked pro
152	19	15.6	20	2	S23742	tet leader peptide	225	18	14.8	18	2	T08159	hypothetical prote
153	19	15.6	20	2	T26748	hypothetical prote	226	18	14.8	18	2	A35678	L-lactate dehydrog
154	19	15.6	20	2	C49404	T-cell receptor be	227	18	14.8	19	2	I49422	integrin alpha-7 c
155	19	15.6	20	2	S29636	superoxide dismuta	228	18	14.8	19	2	A41668	hypothetical prote
156	19	15.6	20	2	PQ0732	lamin B receptor -	229	18	14.8	19	2	PC1322	phosphonoacetaldeh
157	19	15.6	20	2	S28405	metalloproteinase	230	18	14.8	19	2	S63510	hypothetical prote
158	19	15.6	20	2	A58903	H+-transporting tw	231	18	14.8	20	2	PC1324	creatine kinase (E
159	19	15.6	21	2	B35473	T-cell receptor J-	232	18	14.8	20	2	A53875	collagenolytic pro
160	19	15.6	21	2	S47205	sperm chromatin pr	233	18	14.8	20	2	B34817	collagenolytic pro
161	19	15.6	21	2	PN0082	hypothetical 2.5K	234	18	14.8	20	2	C34817	collagen alpha 5(I
162	19	15.6	21	2	JQ2196	Ig heavy chain DJ	235	18	14.8	20	2	B39419	serum amyloid p-co
163	19	15.6	21	2	PH1369	probable nitrate r	236	18	14.8	20	2	A05332	carbon-monoxide de
164	19	15.6	21	2	S61306	interleukin-7 rece	237	18	14.8	20	2	FL0145	hypothetical prote
165	19	15.6	22	2	B40256	T-cell receptor J-	238	18	14.8	20	2	B30208	major outer membra
166	19	15.6	22	2	S47193	probable antigen 6	239	18	14.8	20	2	S28434	nikkomycin synthet
167	19	15.6	22	2	F41476	collagen alpha 3(I	240	18	14.8	20	2	S61378	glutathione-bindin
168	19	15.6	22	2	S64675	L-serine dehydrata	241	18	14.8	20	2	S53440	ribosomal protein
169	19	15.6	22	2	S16224	translation initia	242	18	14.8	20	2	S78759	collagen alpha 1(I
170	19	15.6	22	2	PT0052	hypothetical prote	243	18	14.8	21	2	A39543	glyceraldehyde-3-p
171	19	15.6	22	2	F84018	T-cell receptor J-	244	18	14.8	21	2	S12055	4-hydroxybenzoate
172	19	15.6	23	2	S47191	T-cell receptor J-	245	18	14.8	21	2	PT0089	carbanic anhydrase
173	19	15.6	23	2	S47210	T-cell receptor be	246	18	14.8	21	2	S48632	translational elonga
174	19	15.6	23	2	S07967	nucleoside-diphosp	247	18	14.8	21	2	A20359	collagen alpha 3(I
175	19	15.6	24	2	S47563		248	18	14.8	21	2	C39543	

249 18 14.8 22 2 B60475 Glyceraldehyde-3-p
250 18 14.8 22 2 JN0911 N4-(beta-N-acetyl

ALIGNMENTS

RESULT 1
S65399
immunodeficiency virus type 1, HIV-1 gp120 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S65399
R;Niwa, Y.; Yano, M.; Futaki, S.; Okumura, Y.; Kido, H.
Eur. J. Biochem. 237, 64-70, 1996
A;Title: T-cell membrane-associated serine protease, tryptase TL(2), binds human immunod
man immunodeficiency virus type 1 inhibit cleavage of gp120.
A;Reference number: S65399; MUID:96203909; PMID:8620895
A;Accession: S65399
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10;11-20 <NIW>
C;Superfamily: type E retrovirus env polyprotein

Query Match 52.5%; Score 64; DB 2; Length 20;
Best Local Similarity 92.3%; Pred. No. 0.001;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RGPGRFVTIGKI 23
Db 1 RGPGRFVTIGRI 13

RESULT 2
S66213
Glucose 1-dehydrogenase (EC 1.1.1.47) - Haloferax mediterranei (fragment)
C;Species: Haloferax mediterranei
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66213
R;Bonete, M.J.; Bire, C.; Llorca, F.I.; Camacho, M.L.
FEBS Lett. 383, 227-229, 1996
A;Title: Glucose dehydrogenase from the halophilic Archaeon Haloferax mediterranei: enzy
A;Reference number: S66213; MUID:96198607; PMID:8925901
A;Accession: S66213
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BN>
A;Cross-references: UNIPROT:Q977U7
C;Keywords: oxidoreductase

Query Match 23.8%; Score 29; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 4.2e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 5 KSRIQPGGRAFV 18
Db 2 KAIAVKRGEDRPV 15

RESULT 3
S48654
Plasmepein II - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jun-2000
C;Accession: S48654
R;Hill, J.; Tyas, L.; Phyllip, L.H.; Kay, J.; Dunn, B.M.; Berry, C.
FEBS Lett. 352, 155-158, 1994
A;Title: High level expression and characterisation of Plasmepein II, an aspartic prote
A;Reference number: S48654; MUID:95010698; PMID:7925966
A;Accession: S48654
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-20 <HIL>

Query Match 22.1%; Score 27; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 10 ORGPGRAFVTIG 21
Db 9 QMGRGSEHLTIG 20

RESULT 4
PA0109
porin por 1B - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: PA0109
R;Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A;Reference number: PA0109
A;Accession: PA0109
A;Molecule type: protein
A;Residues: 1-14 <KAM>
A;Cross-references: UNIPROT:Q8LA84; UNIPROT:Q42292
A;Experimental source: root

Query Match 21.7%; Score 26.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 11 RGPGRFVTIGK 22
Db 2 KGFG-LYTEIGK 12

RESULT 5
PA0045
porin por1 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: PA0045
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensio
A;Reference number: PA0001
A;Accession: PA0045
A;Molecule type: protein
A;Residues: 1-14 <KAM>
A;Cross-references: UNIPROT:Q7M1W9
A;Experimental source: root

Query Match 21.7%; Score 26.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 11 RGPGRFVTIGK 22
Db 2 KGFG-LYTEIGK 12

RESULT 6
S03879
6-phosphofructokinase (EC 2.7.1.11) B - rabbit (fragment)
N;Alternate names: phosphofructo-1-kinase B
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S03879
R;Valatis, A.P.; Foe, L.G.; Kwiatkowska, D.; Latahaw, S.P.; Kemp, R.G.
Biochim. Biophys. Acta 995, 187-194, 1989
A;Title: The sites of phosphorylation of rabbit brain phosphofructo-1-kinase by cyclic A
A;Reference number: S03878; MUID:89194250; PMID:2539199
A;Accession: S03879
A;Molecule type: protein
A;Residues: 1-13 <VAL>

A;Cross-references: UNIPROT:Q7M3F5
 A;Note: the sequence from the summary is inconsistent with that from table I and Fig. 4
 C;Keywords: glycolysis; phosphotransferase

Query Match 21.3%; Score 26; DB 2; Length 13;
 Best Local Similarity 40.0%; Pred. No. 1e+03;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 TRKSIRIQRG 12
 |||:|:|:|:
 Db 3 TRRSLSMDKG 12

RESULT 7
 D28027
 protein P7 - curled-leaved tobacco (fragment)
 C;Species: Nicotiana glauca (curled-leaved tobacco)
 C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C;Accession: D28027
 R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
 A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid
 A;Reference number: A94167
 A;Accession: D28027
 A;Molecule type: protein
 A;Residues: 1-10 <BAU>
 A;Cross-references: UNIPROT:Q7M1V8

Query Match 20.5%; Score 25; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 GRAFVTI 20
 |||:|:|:
 Db 3 GRSEFPI 9

RESULT 8
 S11286
 exo-alpha-sialidase (EC 3.2.1.18) - influenza A virus (strain A/FPV/Rostock/34 [H7N1])
 N;Alternate names: neuraminidase
 C;Species: influenza A virus
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
 C;Accession: S11286
 R;Robertson, J.S.
 Nucleic Acids Res. 6, 3745-3757, 1979
 A;Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza
 A;Reference number: S11286; MUID:80034428; PMID:493121
 A;Accession: S11286
 A;Molecule type: genomic RNA
 A;Residues: 1-12 <ROB>
 A;Cross-references: EMBL:J02114; NID:G324483; PIDN:AAA43398.1; PID:G324486
 C;Genetics:
 A;Map position: segment 6
 C;Superfamily: influenza virus exo-alpha-sialidase
 C;Keywords: glycosidase; hydrolase

Query Match 20.5%; Score 25; DB 2; Length 12;
 Best Local Similarity 44.4%; Pred. No. 1.3e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 13 PGRAFVTIG 21
 |||:|:|:
 Db 3 FNQKIITIG 11

RESULT 9
 JN0264
 translation initiation factor eIF-2 gamma chain - pig (fragment)
 N;Alternate names: eIF2 gamma chain
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
 C;Accession: JN0264

R;Mukoyama, E.B.; Shikawa, H.; Suzuki, H.
 Biosci. Biotechnol. Biochem. 56, 680-681, 1992
 A;Title: GTP-binding sequences in the gamma subunit of pig liver initiation factor 2.
 A;Reference number: JN0264; MUID:92282179; PMID:1368212
 A;Accession: JN0264
 A;Molecule type: protein
 A;Residues: 1-16 <MUK>
 A;Cross-references: UNIPROT:Q9TRQ9
 A;Experimental source: liver
 C;Keywords: GTP binding
 F;1-16/Region: GTP binding #status experimental

Query Match 20.5%; Score 25; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 RAFVTICKIG 24
 |||:|:|:
 Db 1 QATINIGTIG 10

RESULT 10
 A37823
 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
 C;Accession: A37823
 R;Rahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.
 J. Biol. Chem. 265, 14512-14517, 1990
 A;Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon select
 A;Reference number: A37823; MUID:90354445; PMID:2167319
 A;Accession: A37823
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-17 <RAH>
 A;Cross-references: UNIPROT:Q7M2M8
 C;Keywords: acyltransferase; coenzyme A

Query Match 20.1%; Score 24.5; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 2.3e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 12 GP-GRFVIT 19
 |||:|:|:
 Db 1 GPKGRVFVS 9

RESULT 11
 PT0515
 T-cell receptor beta chain V-D-J region (100-4AE) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0515
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0515
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-7 <FEE>
 A;Experimental source: adult thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 19.7%; Score 24; DB 2; Length 7;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPGRA 16
 |||:|:|:
 Db 3 GPGQA 7

RESULT 12

C53275
Ig kappa-1 chain J3 segment b95 allotype - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C:Accession: C53275
R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991
A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A:Reference number: A53275; MUID:91372868; PMID:1909995
A:Accession: C53275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <AYA>
A:Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBI:56164)
C:Comment: This J3 segment may not be functional because of substitutions in the 7 mer a
C:Keywords: heterotetramer; immunoglobulin

Query Match 19.7%; Score 24; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RGGP 14

Db 3 RGGP 6

RESULT 13

PH0915
T-cell receptor beta chain V-D-J region (isolate 1) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0915
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A:Reference number: PH0915; MUID:92078857; PMID:1836012
A:Accession: PH0915
A:Molecule type: mRNA
A:Residues: 1-14 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
A:Note: the authors translated the codon GGG for residue 8 as Glu and GAG for residue 9
C:Keywords: T-cell receptor

Query Match 19.7%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 QRGPGRAF 17

Db 4 RRGTGAV 11

RESULT 14

S63490
dissimilatory sulfite reductase alpha chain, soluble - Desulfovibrio desulfuricans (frag
C:Species: Desulfovibrio desulfuricans
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S63490
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio
A:Reference number: S63489; MUID:96085152; PMID:8521853
A:Accession: S63490
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <STE>
A:Cross-references: UNIPROT:Q9R4H4

Query Match 19.7%; Score 24; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 3.2e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 RIORGPGRAFV 18
Db 10 QLESGPWPSEV 20

RESULT 15

S31427
biliary glycoprotein - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-Feb-1997
C:Accession: S31427
R:Nedellec, P.; Turbide, C.; Barnett, T.R.; Beauchemin, N.
submitted to the EMBL data library, July 1992
A:Description: Characterization of the human biliary glycoprotein regulatory region.
A:Reference number: S31427
A:Accession: S31427
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-21 <NED>
A:Cross-references: EMBL:X67277
C:Keywords: glycoprotein

Query Match 19.7%; Score 24; DB 2; Length 21;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 PGRAF 17

Db 14 PGRGF 18

Search completed: June 3, 2005, 03:21:13
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 03:03:22 ; Search time 171 Seconds
(without alignments)
71.871 Million cell updates/sec

Title: SEQ1

Perfect score: 122

Sequence: 1 nntksirirgpggrafvtigkig 24

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 16988

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 250 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	65	53.3	23	2	Q9E8S7
2	63	51.6	25	2	Q9AQX9
3	63	51.6	25	2	Q9AQX9
4	59	48.4	25	2	O10481
5	53	43.4	25	2	Q9AQY1
6	53	43.4	25	2	Q9AQY2
7	51	41.8	25	2	Q9QEX7
8	45	36.9	25	2	Q7ZJT3
9	39	32.0	18	2	Q9PXF1
10	38	31.1	23	2	Q9ENM9
11	33	27.0	22	2	O6U2M7
12	29	23.8	20	2	Q7R974
13	28	23.0	24	2	Q9RQ46
14	28	23.0	16	2	Q9R4L1
15	27	22.1	16	2	Q9UCK9
16	27	22.1	16	2	Q9UCL0
17	27	22.1	17	2	Q16228
18	27	22.1	19	2	Q6EMJ0
19	27	22.1	19	2	Q6EMJ1
20	27	22.1	22	2	Q924C7
21	26.5	21.7	14	2	Q7M1W9
22	26	21.3	13	2	Q7M3F5
23	26	21.3	14	2	Q7PE81
24	26	21.3	17	2	Q9R5N0
25	26	21.3	17	2	Q78324
26	26	21.3	18	2	Q9ZG65
27	26	21.3	20	2	Q6JCN3
28	26	21.3	21	2	Q95K54
29	26	21.3	21	2	Q6RCX2
30	26	21.3	22	2	Q72922
31	26	21.3	23	2	Q6U2M9

32	26	21.3	24	2	Q6TQT6	Q6TQT6	saccharomyc
33	26	21.3	24	2	Q6U2N2	Q6U2N2	citrullus l
34	26	21.3	24	2	Q9RQ50	Q9RQ50	buchnera ap
35	26	21.3	25	2	Q69EY6	Q69EY6	lycopersico
36	25	20.5	10	2	Q7M1V8	Q7M1V8	nicotiana p
37	25	20.5	12	2	Q84038	Q84038	influenza a
38	25	20.5	13	2	Q6TUI7	Q6TUI7	ascaris suu
39	25	20.5	14	2	Q9P2A2	Q9P2A2	homo sapien
40	25	20.5	14	2	Q85662	Q85662	reovirus ty
41	25	20.5	15	2	Q86576	Q86576	subterranea
42	25	20.5	16	2	Q9UCJ7	Q9UCJ7	homo sapien
43	25	20.5	16	2	Q9TRQ9	Q9TRQ9	scrofa
44	25	20.5	17	2	Q78326	Q78326	human immun
45	25	20.5	19	2	Q90630	Q90630	cercopithe
46	25	20.5	19	2	Q90633	Q90633	cercopithe
47	25	20.5	19	2	Q90R12	Q90R12	human immun
48	25	20.5	20	2	Q9PW04	Q9PW04	gallus gall
49	25	20.5	22	2	Q6V0X7	Q6V0X7	serratia ma
50	25	20.5	22	2	Q9AH71	Q9AH71	neisseria m
51	25	20.5	24	1	FCLJ_PACGO	FCLJ_PACGO	pachycondyl
52	25	20.5	24	1	FCL2_PACGO	FCL2_PACGO	pachycondyl
53	24.5	20.1	17	2	Q7M2M8	Q7M2M8	bos taurus
54	24.5	20.1	24	2	Q89021	Q89021	mus musculu
55	24.5	20.1	25	2	Q9TWN6	Q9TWN6	theileria s
56	24	19.7	11	2	Q7S0C5	Q7S0C5	neurospora
57	24	19.7	15	2	Q8TCS7	Q8TCS7	homo sapien
58	24	19.7	15	2	Q69173	Q69173	yersinia pe
59	24	19.7	16	2	Q48387	Q48387	klebsiella
60	24	19.7	17	2	Q78345	Q78345	human immun
61	24	19.7	17	2	Q78378	Q78378	human immun
62	24	19.7	19	2	Q84859	Q84859	unidentifie
63	24	19.7	19	2	Q8U0H2	Q8U0H2	gallus gall
64	24	19.7	19	2	Q8UVE0	Q8UVE0	gallus gall
65	24	19.7	20	2	Q7RM33	Q7RM33	plasmodium
66	24	19.7	20	2	Q9R4H4	Q9R4H4	desulfovibr
67	24	19.7	21	1	CSPS_STRTR	CSPS_STRTR	streptococc
68	24	19.7	24	2	Q9R4A4	Q9R4A4	orskovia x
69	24	19.7	25	1	BLP4_BOMOR	BLP4_BOMOR	bombina ori
70	24	19.7	25	1	OCE1_LEFOE	OCE1_LEFOE	leptodactyl
71	23.5	19.3	16	2	Q8JH96	Q8JH96	anthus spin
72	23.5	19.3	16	2	Q8JH97	Q8JH97	anthus prat
73	23.5	19.3	21	2	Q9TRK1	Q9TRK1	canis fami
74	23.5	19.3	22	2	Q85524	Q85524	chlamydia t
75	23	18.9	10	1	COXO_RAT	COXO_RAT	rattus norv
76	23	18.9	15	1	UC19_MAIZE	UC19_MAIZE	zea mays (m
77	23	18.9	15	2	Q6TXW1	Q6TXW1	babesia ovi
78	23	18.9	15	2	Q7WUF8	Q7WUF8	pseudomonas
79	23	18.9	16	2	Q6XA08	Q6XA08	equus cabal
80	23	18.9	17	1	FATS_ANASP	FATS_ANASP	anabaena sp
81	23	18.9	17	2	Q91352	Q91352	gallus gall
82	23	18.9	17	2	Q78374	Q78374	human immun
83	23	18.9	17	2	Q78381	Q78381	human immun
84	23	18.9	19	1	TRP3_LEUMA	TRP3_LEUMA	leucophaea
85	23	18.9	20	2	Q51558	Q51558	pseudomonas
86	23	18.9	20	2	Q7M195	Q7M195	thermus aqu
87	23	18.9	21	2	Q46419	Q46419	chlamydia t
88	23	18.9	22	2	Q7S0M0	Q7S0M0	neurospora
89	23	18.9	22	2	Q9R4Y8	Q9R4Y8	staphylococ
90	23	18.9	22	2	Q7ZPQ0	Q7ZPQ0	human immun
91	23	18.9	22	2	Q7ZPQ2	Q7ZPQ2	human immun
92	23	18.9	22	2	Q9QEX6	Q9QEX6	human immun
93	23	18.9	23	2	Q61341	Q61341	panulirus i
94	23	18.9	23	2	Q47811	Q47811	trypanosoma
95	23	18.9	23	2	Q9R4U4	Q9R4U4	versinia ps
96	23	18.9	24	2	Q9TRK0	Q9TRK0	bos taurus
97	23	18.9	24	2	Q71J04	Q71J04	lactobacill
98	23	18.9	24	2	Q7M132	Q7M132	treponema h
99	23	18.9	25	1	FLB1_TREHY	FLB1_TREHY	treponema h
100	23	18.4	25	1	SODC_PAROL	SODC_PAROL	paralichthy
101	22.5	18.4	14	1	TKN1_SCHGR	TKN1_SCHGR	schistocerc
102	22.5	18.4	17	2	Q78328	Q78328	human immun
103	22.5	18.4	20	2	Q9U8M6	Q9U8M6	liodrosophi
104	22	18.0	10	2	Q76V19	Q76V19	lactococcu

105	22	18.0	10	2	Q9QVK8	Q9qvks mus sp. mep	178	21	17.2	17	1	MDH ACIDE	P80540 acidovorax
106	22	18.0	14	2	Q16045	Q16045 homo sapien	179	21	17.2	17	2	Q6EML4	Q6eml4 meleagris g
107	22	18.0	14	2	O10226	O10226 human immun	180	21	17.2	17	2	Q6EML5	Q6eml5 gallus gall
108	22	18.0	14	2	O10227	O10227 human immun	181	21	17.2	17	2	Q78323	Q78323 human immun
109	22	18.0	14	2	O10228	O10228 human immun	182	21	17.2	17	2	Q78327	Q78327 human immun
110	22	18.0	14	2	O10232	O10232 human immun	183	21	17.2	17	2	Q78380	Q78380 human immun
111	22	18.0	14	2	O10233	O10233 human immun	184	21	17.2	18	2	Q14042	Q14042 homo sapien
112	22	18.0	15	2	Q66174	Q66174 borrellia ga	185	21	17.2	18	2	Q75M23	Q75m23 mus musculu
113	22	18.0	16	2	Q9TQY6	Q9tqy6 oryctolagus	186	21	17.2	18	2	Q8VDM2	Q8vdm2 mus musculu
114	22	18.0	16	2	Q55090	Q55090 shigella so	187	21	17.2	18	2	Q90790	Q90790 gallus gall
115	22	18.0	17	2	Q9SMC7	Q9smc7 lycopersico	188	21	17.2	18	2	CUCN CUCNA	P84158 cucurbita m
116	22	18.0	17	2	Q9R575	Q9r575 synecocyst	189	21	17.2	19	1	Q8K5B7	P84158 cucurbita m
117	22	18.0	18	1	PCG5_PACGO	P82419 pachycondyl	190	21	17.2	19	2	Q90514	Q90514 human immun
118	22	18.0	19	1	PCG7_PACGO	P82420 pachycondyl	191	21	17.2	20	1	MCRG METTE	P22950 methanosarc
119	22	18.0	19	2	Q55069	Q55069 synecocyst	192	21	17.2	20	2	Q7R9Q5	Q7r9q5 methanodiu
120	22	18.0	19	2	Q62996	Q62996 rattus norv	193	21	17.2	20	2	P92689	P92689 podospira a
121	22	18.0	19	2	Q9CVG4	Q9cvg4 mus musculu	194	21	17.2	20	2	Q9S8H8	Q9s8h8 brassica ra
122	22	18.0	19	2	Q905E4	Q905e4 human immun	195	21	17.2	20	2	Q9SM31	Q9sm31 triticum ae
123	22	18.0	19	2	Q905G4	Q905g4 human immun	196	21	17.2	20	2	Q9SM31	Q9sm31 triticum ae
124	22	18.0	20	1	CD4_SHEEP	P05542 ovis aries	197	21	17.2	20	2	Q8KU19	Q8ku19 rhodococcus
125	22	18.0	20	1	DFTS_RAT	P07448 rattus norv	198	21	17.2	20	2	Q9R4P2	Q9r4p2 brevundimon
126	22	18.0	20	1	EFTU_MYCSY	P81407 mycoplasma	199	21	17.2	20	2	Q8V9H3	Q8v9h3 chicken ane
127	22	18.0	20	2	Q7S7I7	Q7s7i7 neurospora	200	21	17.2	20	2	Q9PXE4	Q9pxe4 foot-and-mo
128	22	18.0	20	2	Q9TRB9	Q9trb9 bos taurus	201	21	17.2	21	2	Q7RCB0	Q7rcb0 plasmodium
129	22	18.0	20	2	Q9TR10	Q9tri0 bos taurus	202	21	17.2	21	2	Q9TU55	Q9tu55 cebus apell
130	22	18.0	20	2	Q6LCU3	Q6lcu3 morganella	203	21	17.2	21	2	Q9LBD3	Q9lbd3 xanthomonas
131	22	18.0	20	2	Q9EQX8	Q9eqx8 mus musculu	204	21	17.2	21	2	Q8K3B6	Q8k3b6 mus musculu
132	22	18.0	21	2	Q9H428	Q9h428 homo sapien	205	21	17.2	21	2	Q8QY55	Q8qy55 polyomaviru
133	22	18.0	21	2	Q64LJ1	Q64lj1 gorilla gor	206	21	17.2	22	2	Q86FQ2	Q86fq2 plasmodium
134	22	18.0	21	2	Q9R890	Q9r890 chlamydia t	207	21	17.2	22	2	Q37940	Q37940 lactococcus
135	22	18.0	21	2	Q88229	Q88229 mus musculu	208	21	17.2	22	2	Q9SLV6	Q9slv6 nicotiana t
136	22	18.0	21	2	Q9R204	Q9r204 mus musculu	209	21	17.2	22	2	Q6ZXI6	Q6zx16 erwinia amy
137	22	18.0	22	2	P82939	P82939 bordeum vul	210	21	17.2	22	2	Q9R513	Q9r513 porphyromon
138	22	18.0	22	2	Q52435	Q52435 burkholderi	211	21	17.2	22	2	Q89826	Q89826 murine minu
139	22	18.0	22	2	Q6I6B1	Q6i6b1 escherichia	212	21	17.2	22	2	Q9QGE6	Q9qge6 human immun
140	22	18.0	22	2	Q8X365	Q8x365 escherichia	213	21	17.2	22	2	Q9QGE8	Q9qge8 human immun
141	22	18.0	22	2	Q9ZG66	Q9zg66 chlamydia t	214	21	17.2	22	2	Q9QGF0	Q9qgf0 human immun
142	22	18.0	23	2	Q9ZG66	Q9zg66 chlamydia t	215	21	17.2	22	2	Q9QGF6	Q9qgf6 human immun
143	22	18.0	24	1	TFIS_BOMMO	P82204 bombyx mori	216	21	17.2	22	2	Q9QGG0	Q9qgg0 human immun
144	22	18.0	24	1	Q7RJY9	Q7rjy9 plasmodium	217	21	17.2	22	2	Q9QGG8	Q9qgg8 human immun
145	22	18.0	24	2	Q7ZBU6	Q7zbu6 human immun	218	21	17.2	22	2	Q7YRN4	Q7yrn4 bos taurus
146	22	18.0	25	1	RA1C_RANCL	P82875 rana clamit	219	21	17.2	23	2	Q35223	Q35223 oenothera b
147	22	18.0	25	1	RAN1_RANCA	P82741 rana catesb	220	21	17.2	23	2	Q53469	Q53469 mycobacteri
148	22	18.0	25	1	VGT_BPG4	P03652 bacterioph	221	21	17.2	23	2	Q9LA84	Q9la84 rhodobacter
149	22	18.0	25	2	Q7PGE4	Q7pgf4 anopheles g	222	21	17.2	23	2	Q9RA10	Q9ra10 bordetella
150	22	18.0	25	2	Q8MGS5	Q8mjg5 sus scrofa	223	21	17.2	23	2	Q9PSA8	Q9psa8 xenopus bor
151	22	18.0	25	2	Q7M219	Q7m219 triticum tu	224	21	17.2	23	2	Q9QEX4	Q9qex4 human immun
152	22	18.0	25	2	Q60839	Q60839 mus musculu	225	21	17.2	23	2	Q9QEX5	Q9qex5 human immun
153	22	18.0	25	2	Q71UF5	Q71uf5 rattus norv	226	21	17.2	23	2	Q68US7	Q68us7 pan troglod
154	22	18.0	25	2	O11890	O11890 gb virus c/	227	21	17.2	24	2	P81151	P81151 desulfovibr
155	22	18.0	25	2	O11891	O11891 gb virus c/	228	21	17.2	24	2	Q47541	Q47541 escherichia
156	22	18.0	25	2	O11893	O11893 gb virus c/	229	21	17.2	24	2	Q9R573	Q9r573 nitrosomona
157	22	18.0	25	2	Q66MS0	Q66ms0 human immun	230	21	17.2	24	2	BT12_BOOMI	P82357 pseudacanth
158	21.5	17.6	25	2	Q9TQY9	Q9tqy9 sus scrofa	231	21	17.2	24	2	SPIG_PSEUS	Q30045 archaeoglob
159	21.5	17.6	22	2	Q02830	Q02830 oryctolagus	232	21	17.2	25	1	Y194_ARCFU	Q49167 methanobact
160	21.5	17.6	23	2	Q98YR7	Q98yr7 human immun	233	21	17.2	25	2	Q49167	Q49167 plasmodium
161	21.5	17.6	24	2	Q92012	Q92012 mus musculu	234	21	17.2	25	2	Q7RE47	Q7re47 lumbricus t
162	21	17.2	9	2	Q8UCO18	Q8uc38 homo sapien	235	21	17.2	25	2	Q7TWE4	Q7twe4 macaca mula
163	21	17.2	10	1	COXO_THUOB	P80982 thunnus obe	236	21	17.2	25	2	Q77604	Q77604 cercopithec
164	21	17.2	10	2	Q9QVE9	Q9qve9 mus sp. pro	237	21	17.2	25	2	Q77831	Q77831 cercopithec
165	21	17.2	13	2	Q7M1G8	Q7m1g8 avena sativ	238	21	17.2	25	2	Q77832	Q77832 cercopithec
166	21	17.2	14	2	Q47601	Q47601 escherichia	239	21	17.2	25	2	Q8MIA1	Q8mia1 sus scrofa
167	21	17.2	14	2	Q27373	Q27373 trypanosoma	240	21	17.2	25	2	Q8BGJ1	Q8bgj1 tarsius ban
168	21	17.2	15	2	Q7SH11	Q7sh11 neurospora	241	21	17.2	25	2	Q8W0Q3	Q8w0q3 linum usita
169	21	17.2	15	2	Q81ZK4	Q81zk4 homo sapien	242	21	17.2	25	2	Q66RM9	Q66rm9 nevea brasi
170	21	17.2	15	2	Q26825	Q26825 trypanosoma	243	21	17.2	25	2	Q6ZVY1	Q6zyv1 silene ural
171	21	17.2	15	2	P82430	P82430 nicotiana t	244	21	17.2	25	2	Q53499	Q53499 enterobacte
172	21	17.2	15	2	Q93LE6	Q93le6 chloroflexu	245	21	17.2	25	2	Q31ER9	Q31er9 cottontail
173	21	17.2	16	2	Q16350	Q16350 homo sapien	246	21	17.2	25	2	Q9UC7	Q9uc7 homo sapien
174	21	17.2	16	2	Q6JDN2	Q6jdn2 canis famil	247	21	17.2	25	2	Q9EUP4	Q9eup4 thermus the
175	21	17.2	16	2	Q9G0E9	Q9g0e9 bacterioph	248	21	17.2	15	2		
176	21	17.2	16	2	Q47605	Q47605 escherichia	249	20.5	16.8	15	2		
177	21	17.2	16	2	Q71Z16	Q71z16 gallus gall	250	20.5	16.8	17	2		

ALIGNMENTS

RESULT 1
Q9E8S7 Q9E8S7 PRELIMINARY; PRT; 23 AA.
ID Q9E8S7
AC Q9E8S7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20411423; PubMed=10954550;
RX DOI=10.1128/JVI.74.18.8494-8501.2000;
RA Nelson J.A.E., Baribaud F., Edwards T., Swanstrom R.;
RT "Patterns of changes in human immunodeficiency virus type 1 V3
sequence populations late in infection.";
RL J. Virol. 74:8494-8501(2000).
DR EMBL; AF155888; AAG09930.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR011056; Pept_S24_S26_C.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2596 MW; 6C038F27BC0CA1E0 CRC64;

Query Match 53.3%; Score 65; DB 2; Length 23;
Best Local Similarity 60.9%; Pred. No. 0.0019;
Matches 14; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
Qy 1 NNTKRSIRIQGPGRAFVTGKI 23
Db 2 NNTKRSIRIQGPGRAFVTGDI 22

Qy 1 NNTKRSIRIQGPGRAFVTGKI 23
Db 2 NNTKRSIRIQGPGRAFVTGDI 22

RESULT 2
Q8AQX9 Q8AQX9 PRELIMINARY; PRT; 25 AA.
ID Q8AQX9
AC Q8AQX9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22860939; PubMed=14502005;
RX Freil S.A., Fiscus S.A., Pilcher C.D., Menezes P., Giner J.,
RA Patrick E., Lennox J.L., Hicks C.B., Bron J.J. Jr., Shugars D.C.;
RT "Envelope diversity, coreceptor usage and syncytium-inducing phenotype
of HIV-1 variants in saliva and blood during primary infection.";
RL AIDS 17:2025-2033(2003).
DR EMBL; AF536914; AAN63929.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 25
SQ SEQUENCE 25 AA; 2749 MW; 9B6E9DACB8D56C0C CRC64;

Query Match 51.6%; Score 63; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 0.0045;
Matches 15; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTGKI 24
Db 2 NNTKRSIRIQGPGRAFVTGDI 23

RESULT 3
Q8AQY0 Q8AQY0 PRELIMINARY; PRT; 25 AA.
ID Q8AQY0
AC Q8AQY0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22860939; PubMed=14502005;
RX Freil S.A., Fiscus S.A., Pilcher C.D., Menezes P., Giner J.,
RA Patrick E., Lennox J.L., Hicks C.B., Bron J.J. Jr., Shugars D.C.;
RT "Envelope diversity, coreceptor usage and syncytium-inducing phenotype
of HIV-1 variants in saliva and blood during primary infection.";
RL AIDS 17:2025-2033(2003).
DR EMBL; AF536913; AAN63928.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 25
SQ SEQUENCE 25 AA; 2749 MW; 9B6E9DACB8D56C0C CRC64;

Query Match 51.6%; Score 63; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 0.0045;
Matches 15; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTGKI 24
Db 2 NNTKRSIRIQGPGRAFVTGDI 23

RESULT 4
O10481 O10481 PRELIMINARY; PRT; 25 AA.
ID O10481
AC O10481;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97255649; PubMed=9100996;
RX Rencher S.D., Lockey T.D., Slobod K.S., Hurwitz J.L.;
RT "Drift from the GPGRAF HIV-1 envelope V3 crown sequence in a North
American inner city.";
RL AIDS Res. Hum. Retroviruses 13:527-528(1997).
DR EMBL; U81241; AAB53843.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2801 MW; 25EB1B150CD7C14B6 CRC64;

Query Match 48.4%; Score 59; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 0.021;
Matches 14; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 21
Db 6 NNKRKGIHI--GPGAFYTKG 24

RESULT 5
Q8AQY1 PRELIMINARY; PRT; 25 AA.
AC Q8AQY1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=22860939; PubMed=14502005;
RA Freil S.A., Fiscus S.A., Pilcher C.D., Menezes P., Giner J., Shugars D.C.;
RA Patrick E., Lennox J.L., Hicks C.B., Eron J.J. Jr., Shugars D.C.;
RT "Envelope diversity, coreceptor usage and syncytium-inducing phenotype
of HIV-1 variants in saliva and blood during primary infection.";
RL AIDS 17:2025-2033(2003).
DR EMBL; AF536912; AAN63927.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2601 MW; 71B5A774CE256C09 CRC64;

Query Match 43.4%; Score 53; DB 2; Length 25;
Best Local Similarity 58.3%; Pred. No. 0.22;
Matches 14; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 24
Db 2 NNTKGIHI--GPGAFYGTDIIG 23

RESULT 6
Q8AQY2 PRELIMINARY; PRT; 25 AA.
AC Q8AQY2
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=22860939; PubMed=14502005;
RA Freil S.A., Fiscus S.A., Pilcher C.D., Menezes P., Giner J.,
RA Patrick E., Lennox J.L., Hicks C.B., Eron J.J. Jr., Shugars D.C.;
RT "Envelope diversity, coreceptor usage and syncytium-inducing phenotype
of HIV-1 variants in saliva and blood during primary infection.";
RL AIDS 17:2025-2033(2003).
DR EMBL; AF536912; AAN63927.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2601 MW; 71B5A774CE256C09 CRC64;

Query Match 43.4%; Score 53; DB 2; Length 25;
Best Local Similarity 58.3%; Pred. No. 0.22;
Matches 14; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 24
Db 2 NNTKGIHI--GPGAFYGTDIIG 23

RESULT 7
Q9QEX7 PRELIMINARY; PRT; 25 AA.
AC Q9QEX7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=21103026; PubMed=11170057;
RX DOI=10.1002/1096-9071(200103)63:3<197::AID-JMV1000>3.3.CO;2-G;
RA Lin H.J., Siwak E.B., Lauder I.J., Hollinger F.B.;
RT "Long-term culture of human immunodeficiency virus type 1 resulting in
loss of glycosylation sites.";
RL J. Med. Virol. 63:197-202(2001).
DR EMBL; AF178663; AAF04369.1; -.
DR GO; GO:0019021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:vital capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2818 MW; 9C6EBA908EB5ED47 CRC64;

Query Match 41.8%; Score 51; DB 2; Length 25;
Best Local Similarity 57.1%; Pred. No. 0.47;
Matches 12; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 21
Db 7 NNTRSIPL--GQGRAFTTG 25

RESULT 8
Q7ZJT3 PRELIMINARY; PRT; 25 AA.
AC Q7ZJT3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

RL AIDS 17:2025-2033(2003).
DR EMBL; AF536911; AAN63926.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2601 MW; 71B5A774CE256C09 CRC64;

Query Match 43.4%; Score 53; DB 2; Length 25;
Best Local Similarity 58.3%; Pred. No. 0.22;
Matches 14; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 24
Db 2 NNTKGIHI--GPGAFYGTDIIG 23

RESULT 7
Q9QEX7 PRELIMINARY; PRT; 25 AA.
AC Q9QEX7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=21103026; PubMed=11170057;
RX DOI=10.1002/1096-9071(200103)63:3<197::AID-JMV1000>3.3.CO;2-G;
RA Lin H.J., Siwak E.B., Lauder I.J., Hollinger F.B.;
RT "Long-term culture of human immunodeficiency virus type 1 resulting in
loss of glycosylation sites.";
RL J. Med. Virol. 63:197-202(2001).
DR EMBL; AF178663; AAF04369.1; -.
DR GO; GO:0019021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:vital capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2818 MW; 9C6EBA908EB5ED47 CRC64;

Query Match 41.8%; Score 51; DB 2; Length 25;
Best Local Similarity 57.1%; Pred. No. 0.47;
Matches 12; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 21
Db 7 NNTRSIPL--GQGRAFTTG 25

RESULT 8
Q7ZJT3 PRELIMINARY; PRT; 25 AA.
AC Q7ZJT3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22439926; PubMed=12552446;
RA Iversen A.K.N., Christiansen C.B., Attermann J., Eugen-Olsen J.,
RA Schulman S., Berntorp E., Ingerslev J., Fugger L., Scheibel E.,
RA Tengborn L., Gerstoft J., Dickmeis E., Sveigaard A., Skinhoj P.;
RT "Limited protective effect of the CCR5Delta32/CCR5Delta32 genotype on
RT human immunodeficiency virus infection incidence in a cohort of
RL patients with hemophilia and selection for genotypic X4 virus.";
RL J. Infect. Dis. 187:215-225(2003).
DR EMBL; AY150666; AA061698.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 25
SQ SEQUENCE 25 AA; 2790 MW; CB4779D487B698D2 CRC64;

Query Match 36.9%; Score 45; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 4.7;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 8 RIQRGPGRAFTVIGKI 23
Db 1 RLSMGPGRVYVTGPI 16

RESULT 9
Q9PXF1
ID Q9PXF1 PRELIMINARY; PRT; 18 AA.
AC Q9PXF1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GP120 protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RP MEDLINE=95386957; PubMed=7658059;
RA Lawko A., Johansson B., Dash R., Falck L., Dietrich U., Pipkorn R.,
RA Nilehn B., Blomberg J.;
RT "Continuity and discontinuity in the anti-V3 IgG response of human
RT immunodeficiency virus type 1-infected persons in a cross-sectional
RT and longitudinal study using synthetic peptides.";
RL J. Infect. Dis. 172:682-690(1995).
SQ SEQUENCE 18 AA; 2047 MW; F5884C2C32F15B55 CRC64;

Query Match 32.0%; Score 39; DB 2; Length 18;
Best Local Similarity 64.3%; Pred. No. 34;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 NNRKSIRIQRPG 14
Db 7 NNRK--RMTMGPG 18.

RESULT 10
Q9ENM9
ID Q9ENM9 PRELIMINARY; PRT; 23 AA.
AC Q9ENM9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
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RN SEQUENCE FROM N.A.
RX MEDLINE=20411423; PubMed=10954550;
RA DOI=10.1128/JVI.74.18.8494-8501.2000;
RA Nelson J.A.E., Baribaud F., Edwards T., Swanson R.;
RT "Patterns of changes in human immunodeficiency virus type 1 V3
RT sequence populations late in infection.";
RL J. Virol. 74:8494-8501(2000).
DR EMBL; AF092639; AA04382.1; -.
DR GO; GO:0019031; C: viral envelope; IEA.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2460 MW; 6108AEC9C0CA947 CRC64;

Query Match 31.1%; Score 38; DB 2; Length 23;
Best Local Similarity 59.3%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 12 GPGRAFTVIGKI 23
Db 11 GPGKAFVATGDI 22

RESULT 11
Q6U2M7
ID Q6U2M7 PRELIMINARY; PRT; 22 AA.
AC Q6U2M7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Galactinol synthase (EC 2.4.1.123) (Fragment).
GN Name=CAS1;
OS Sechium edule.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Sechium.
OX NCBI_TaxID=184140;
RN SEQUENCE FROM N.A.
RP MEDLINE=22975109; PubMed=14526110; DOI=10.1104/pp.103.027714;
RA Ayre B.G., Blair J.E., Turgeon R.;
RT "Functional and phylogenetic analyses of a conserved regulatory
RT program in the phloem of minor veins.";
RL Plant Physiol. 133:1229-1239(2003).
DR EMBL; AV379782; AA074884.1; -.
DR GO; GO:0047216; F: inositol 3-alpha-galactosyltransferase acti. . .; IEA.
DR GO; GO:0016757; F: transferase activity, transferring glycosyl. . .; IEA.
KW Glycosyltransferase; Transferase.
FT NON_TER 22
SQ SEQUENCE 22 AA; 2295 MW; A6673B5BFD06430C CRC64;

Query Match 27.0%; Score 33; DB 2; Length 22;
Best Local Similarity 47.1%; Pred. No. 4.3e+02;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 TRKSIRIQRPGRAFTV 19
Db 6 TETAESTDAPKRAFTV 22

RESULT 12
Q7R974
ID Q7R974 PRELIMINARY; PRT; 20 AA.
AC Q7R974;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=Py06991;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
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RN  SEQUENCE FROM N.A.
RC  STRAIN=17XNL;
RX  PubMed=12368865; DOI=10.1038/nature01099;
RA  Carlton J.M., Anguillo S.V., Suh B.B., Kooij T.W., Perteau M.,
RA  Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA  Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA  Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA  Cho J.K., Quackenbush J., Sedegh M., Shoaibi A., Cummings L.M.,
RA  Florens L., Yates F.R. II, Raine J.D., Sinden R.E., Harris M.A.,
RA  Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA  van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA  Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA  Carucci D.J.;
RT  "Genome sequence and comparative analysis of the model rodent malaria
RT  parasite Plasmodium yoelii yoelii."
RL  Nature 419:512-519(2002).
CC  -1- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL: AABL01002466; EAA19325.1; -.
KW  Hypothetical protein.
FT  NON_TER 20
SQ  SEQUENCE 20 AA; 2461 MW; CS83B1AD3845C3FC CRC64;

Query Match 23.8%; Score 29; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 IRIQGGGPGAPV 18
Db 9 INMKRGTSRLFI 20

RESULT 13
ID Q9RQ46 PRELIMINARY; PRT; 24 AA.
AC Q9RQ46;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP-dependent DNA helicase (Fragment).
GN Name=rep;
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;

[1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=20022990; PubMed=10555290;
RA  Clark M.A., Moran N.A., Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
RT  compositions."
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR  EMBL: AF130814; AAF13808.1; -.
DR  GO; GO:0005524; F:ATP binding; IEA.
DR  GO; GO:0004003; F:ATP-dependent DNA helicase activity; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  GO; GO:0004386; F:helicase activity; IEA.
DR  GO; GO:0006281; P:DNA repair; IEA.
DR  InterPro: IPR000212; UvrD-helicase.
DR  Pfam: PF00580; UvrD-helicase; 1.
KW Helicase.
FT NON_TER 24
SQ  SEQUENCE 24 AA; 2515 MW; EA88246B840C4B75 CRC64;

Query Match 23.8%; Score 29; DB 2; Length 24;
Best Local Similarity 41.7%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NTRKSIRIQGP 13
Db 6 NQKXAVRCISGP 17
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RESULT 14
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AC Q9R4L1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE L-lactate dehydrogenase homolog (Fragment).
OS Spiroplasma melliferum.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Spiroplasmataceae; Spiroplasma.
OX NCBI_TaxID=21134;

[1]
RN  SEQUENCE.
RX  MEDLINE=95331240; PubMed=7607178;
RA  Cordwell S.J., Wilkins M.R., Cerpa-Poljak A., Gooley A.A., Duncan M.,
RA  Williams K.L., Humphrey-Smith I.;
RL Electrophoresis 16:438-443(1995).
SQ  SEQUENCE 16 AA; 1749 MW; FF2078A15AE1647C CRC64;

Query Match 23.0%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NNTRKSIRIQRG 12
Db 3 NSTRKVLVLEG 14

RESULT 15
ID Q9UCK9 PRELIMINARY; PRT; 16 AA.
AC Q9UCK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serum amyloid A isotype 2 alpha protein (Serum amyloid A protein)
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

[1]
RN  SEQUENCE.
RX  MEDLINE=93099171; PubMed=1463770; DOI=10.1016/0925-4439(92)90068-X;
RA  Baba S., Takahashi T., Kasama T., Shirasawa H.;
RT "Identification of two novel amyloid A protein subsets coexisting in
RT  an individual patient of AA-amyloidosis."
RL Biochim. Biophys. Acta 1180:195-200(1992).
DR  PIR; A27902; YLHUA.
DR  GO; GO:0005576; C:extracellular; IEA.
DR  GO; GO:0006953; P:acute-phase response; IEA.
DR  InterPro: IPR000096; Serum_amyloid_A.
DR  Pfam: PF00277; SAA; 1.
SQ  SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8CC1 CRC64;

Query Match 22.1%; Score 27; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 RGPGRAP 17
Db 1 RGPGGAW 7
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Search completed: June 3, 2005, 03:20:35
Job time : 183 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 03:12:32 ; Search time 40 Seconds
(without alignments)
44.789 Million cell updates/sec

Title: SEQ1
Perfect score: 122
Sequence: 1 nntksirigpgrafvtgkig 24

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 218077

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 250 summaries

Database : Issued Patents AA.*
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4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	122	100.0	24	1	US-08-097-751-1
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3	122	100.0	24	2	US-08-146-028-160
4	122	100.0	24	3	US-08-723-425A-160
5	122	100.0	24	3	US-08-480-332-2
6	122	100.0	24	3	US-09-112-206-160
7	122	100.0	24	4	US-09-790-497A-14
8	122	100.0	24	4	US-08-790-497A-160
9	122	100.0	24	4	US-09-576-824A-160
10	122	100.0	24	4	US-09-680-497-160
11	122	100.0	24	5	PCT-US92-06688-12
12	122	100.0	24	5	PCT-US92-10378-3
13	122	100.0	25	3	US-08-465-324-13
14	122	100.0	25	3	US-08-485-324-31
15	122	100.0	25	3	US-08-447-506-13
16	122	100.0	25	3	US-08-447-506-31
17	122	100.0	25	3	US-08-235-437-13
18	122	100.0	25	3	US-08-235-437-31
19	122	100.0	25	3	US-08-447-515-13
20	122	100.0	25	3	US-08-447-515-31
21	116	95.1	24	1	US-08-257-528B-99
22	116	95.1	24	1	US-08-460-602A-99
23	116	95.1	24	1	US-08-463-966A-99
24	116	95.1	24	1	US-08-465-217A-99
25	116	95.1	24	2	US-08-464-329A-99
26	116	95.1	24	2	US-08-462-507A-99
27	116	95.1	24	2	US-08-467-881A-99

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29	112	91.8	25	2	US-07-950-571A-1	Sequence 1, Appli
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31	108	88.5	22	2	US-08-537-245-1	Sequence 1, Appli
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33	106	86.9	22	3	US-09-070-291-5	Sequence 5, Appli
34	101	82.8	21	2	US-08-452-503A-4	Sequence 4, Appli
35	101	82.8	21	2	US-08-453-745A-4	Sequence 4, Appli
36	101	82.8	21	2	US-08-470-419-25	Sequence 25, Appli
37	101	82.8	21	2	US-08-761-828-25	Sequence 25, Appli
38	101	82.8	21	2	US-08-452-520B-4	Sequence 4, Appli
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42	101	82.8	21	3	US-09-027-955-25	Sequence 25, Appli
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45	101	82.8	21	4	US-09-635-754-25	Sequence 25, Appli
46	101	82.8	21	4	US-08-680-525-25	Sequence 25, Appli
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53	101	82.8	25	2	US-08-493-235-23	Sequence 23, Appli
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57	99	81.1	20	4	US-09-813-659-3	Sequence 3, Appli
58	99	81.1	20	4	US-09-549-067A-3	Sequence 3, Appli
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60	97	79.5	23	2	US-08-657-392-27	Sequence 27, Appli
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62	96	78.7	20	1	US-08-257-528B-51	Sequence 51, Appli
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65	96	78.7	20	2	US-08-465-217A-51	Sequence 51, Appli
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88	85	69.7	17	1	US-08-465-217A-35	Sequence 35, Appli
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103	77	63.1	15	1	US-08-218-025A-17	Sequence 17, Appl	176	73	59.8	25	3	US-09-112-206-9	Sequence 9, Appl
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107	77	63.1	15	1	US-08-095-332-1	Sequence 1, Appl	180	72	59.0	14	2	US-08-455-625-9	Sequence 9, Appl
108	77	63.1	15	1	US-08-707-801A-7	Sequence 7, Appl	181	72	59.0	14	3	US-08-455-685-9	Sequence 9, Appl
109	77	63.1	15	1	US-08-709-006-7	Sequence 7, Appl	182	72	59.0	14	3	US-08-060-988A-9	Sequence 9, Appl
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118	77	63.1	15	2	US-08-395-204-2	Sequence 2, Appl	191	72	59.0	15	3	US-08-060-988A-19	Sequence 19, Appl
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121	77	63.1	15	2	US-08-986-234-13	Sequence 13, Appl	194	72	59.0	15	5	PCT-US94-05142-20	Sequence 20, Appl
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126	77	63.1	15	3	US-08-455-685-7	Sequence 7, Appl	199	71	58.2	15	2	US-08-455-625-13	Sequence 13, Appl
127	77	63.1	15	3	US-08-060-988A-7	Sequence 7, Appl	200	71	58.2	15	2	US-08-455-625-15	Sequence 15, Appl
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132	77	63.1	15	5	PCT-US92-10378-1	Sequence 1, Appl	205	71	58.2	15	3	US-08-455-685-15	Sequence 15, Appl
133	77	63.1	15	5	PCT-US94-05142-7	Sequence 7, Appl	206	71	58.2	15	3	US-08-455-685-16	Sequence 16, Appl
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135	76	62.3	15	1	US-08-704-170-72	Sequence 72, Appl	208	71	58.2	15	3	US-08-455-685-22	Sequence 22, Appl
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137	76	62.3	23	3	US-08-513-968-74	Sequence 74, Appl	210	71	58.2	15	3	US-08-060-988A-13	Sequence 13, Appl
138	76	62.3	23	3	US-08-513-968-75	Sequence 75, Appl	211	71	58.2	15	3	US-08-060-988A-15	Sequence 15, Appl
139	76	62.3	23	4	US-08-730-497A-154	Sequence 154, App	212	71	58.2	15	3	US-08-060-988A-16	Sequence 16, Appl
140	76	62.3	23	4	US-08-576-824A-154	Sequence 154, App	213	71	58.2	15	3	US-08-060-988A-18	Sequence 18, Appl
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143	76	62.3	25	3	US-08-723-425A-7	Sequence 7, Appl	216	71	58.2	15	5	PCT-US94-05142-13	Sequence 13, Appl
144	76	62.3	25	3	US-08-723-425A-154	Sequence 154, App	217	71	58.2	15	5	PCT-US94-05142-15	Sequence 15, Appl
145	76	62.3	25	3	US-09-112-206-7	Sequence 7, Appl	218	71	58.2	15	5	PCT-US94-05142-16	Sequence 16, Appl
146	76	62.3	25	3	US-09-112-206-154	Sequence 154, App	219	71	58.2	15	5	PCT-US94-05142-18	Sequence 18, Appl
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148	76	62.3	25	4	US-09-680-497-154	Sequence 154, App	221	71	58.2	15	5	PCT-US94-05142-22	Sequence 22, Appl
149	75	61.5	15	1	US-08-704-170-70	Sequence 70, Appl	222	71	58.2	24	1	US-08-218-025A-134	Sequence 134, App
150	75	61.5	15	5	PCT-US94-02631-70	Sequence 70, Appl	223	71	58.2	24	1	US-08-306-116A-16	Sequence 16, Appl
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158	73	59.8	14	1	US-08-090-148-4	Sequence 4, Appl	231	69	56.6	15	3	US-08-455-685-14	Sequence 14, Appl
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167	73	59.8	22	3	US-08-513-968-72	Sequence 72, Appl	240	68	55.7	22	2	US-08-345-321-22	Sequence 22, Appl
168	73	59.8	23	3	US-09-790-497A-155	Sequence 155, App	241	68	55.7	22	4	US-09-790-497A-7	Sequence 7, Appl
169	73	59.8	23	4	US-09-576-824A-155	Sequence 155, App	242	66.5	54.5	22	4	US-09-576-824A-9	Sequence 9, Appl
170	73	59.8	24	2	US-08-345-321-12	Sequence 12, Appl	243	66.5	54.5	24	4	US-09-576-824A-9	Sequence 9, Appl
171	73	59.8	25	2	US-08-146-028-9	Sequence 9, Appl	244	66	54.1	13	1	US-08-488-252-25	Sequence 25, Appl
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247 66 54.1 13 2 US-08-657-392-20 Sequence 20, Appl
 248 66 54.1 13 2 US-08-657-392-21 Sequence 21, Appl
 249 66 54.1 13 2 US-08-657-392-23 Sequence 23, Appl
 250 66 54.1 13 5 PCT-US94-02539-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
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 ; Sequence 1, Application US/08097751
 ; Patent No. 5527666
 ; GENERAL INFORMATION:
 ; APPLICANT: Derossi, Anita
 ; APPLICANT: Pasti, Marcella
 ; APPLICANT: Mammano, Fabrizio
 ; APPLICANT: Panozzo, Maria
 ; APPLICANT: Dettin, Monica
 ; APPLICANT: DiBello, Carlo
 ; APPLICANT: Chiesco-Bianchi, Luigi
 ; TITLE OF INVENTION: METHOD FOR THE DIAGNOSIS IN VITRO OF
 ; TITLE OF INVENTION: HIV-1 VIRUS INFECTIONS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hedman, Gibson, Costigan & Hoare
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/097,751
 ; FILING DATE: 19930723
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Costigan, James V.
 ; REGISTRATION NUMBER: 25,669
 ; REFERENCE/DOCKET NUMBER: 515-4026
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 302-8989
 ; TELEFAX: (212) 302-8998
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: circular
 ; US-08-097-751-1
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 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 DB 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 RESULT 2
 US-08-090-148-6
 ; Sequence 6, Application US/08090148
 ; Patent No. 5534257
 ; GENERAL INFORMATION:
 ; APPLICANT: Mastico, Robert Allan
 ; APPLICANT: Stockley, Peter George

APPLICANT: Talbot, Simon John
 TITLE OF INVENTION: Antigen-Presenting Capsid with
 TITLE OF INVENTION: Fusion MS2-Coat Protein
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rosenman & Colin
 STREET: 575 Madison Avenue
 CITY: New York
 STATE: NY
 COUNTRY: U.S.A.
 ZIP: 10022-2585
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5", 1.44Mb
 COMPUTER: IBM PS2-486
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/090,148
 FILING DATE: 08/11/93
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9101550.3
 FILING DATE: 01/24/93
 APPLICATION NUMBER: PCT/GB92/00124
 FILING DATE: 01/22/92
 ATTORNEY/AGENT INFORMATION:
 NAME: Nissenbaum, Israel
 REGISTRATION NUMBER: 27,582
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 940-8636
 TELEFAX: (212) 940-6404
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 AMINO ACIDS
 TYPE: AMINO ACID
 TOPOLOGY: NOT RELEVANT
 MOLECULE TYPE: PEPTIDE
 US-08-090-148-6
 Query Match 100.0%; Score 122; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 RESULT 3
 US-08-146-028-160
 ; Sequence 160, Application US/08146028
 ; Patent No. 5891640
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
 ; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
 ; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
 ; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
 ; NUMBER OF SEQUENCES: 453
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/146,028
 ; INFORMATION FOR SEQ ID NO: 160:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single


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; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00231/052W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: AMINO ACID
; TOPOLOGY: linear
;
PCT-US92-06688-12
;
Query Match 100.0%; Score 122; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps
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DDB 1 NNRKSIQRGPGRAFTVIGKIG 24
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; Sequence 3, Application PC/TUS9210378
; GENERAL INFORMATION:
; APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF
; APPLICANT: TEXAS SYSTEM
; APPLICANT: SASTRY, Jagannadha K.
; APPLICANT: ARLINGHAUS, Ralph B.
; APPLICANT: PLATSOUCAAS, Chris D.
; APPLICANT: NEHETE, Pramod N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: FOR ELICITING IMMUNE OR ANTI-INFECTION RESPONSES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: WordPerfect 5.1
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; APPLICATION NUMBER: PCT/US92/10378
; FILING DATE: 19921202
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/800,932
; FILING DATE: December 2, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/945865
; FILING DATE: September 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTPC305PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; TELEX: Not Applicable
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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PCT-US92-10378-3

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 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 NNTKSIIRIQGPGRAFTVIGKIG 24

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 ; Patent No. 6043093
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlstadter, Jacob
 ; TITLE OF INVENTION: SELECTION METHODS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Curtis, Morris, & Safford
 ; ADDRESSEE: c/o Barry Evans
 ; STREET: 530 Fifth Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,324
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/235,437
 ; FILING DATE: 29-APR-1994
 ; APPLICATION NUMBER: US 07/852,412
 ; FILING DATE: 16-MAR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Evans, Barry
 ; REGISTRATION NUMBER: 22,802
 ; REFERENCE/DOCKET NUMBER: 370132-2000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 840-3333
 ; TELEFAX: (212) 840-0712
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-485-324-13

Query Match 100.0%; Score 122; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
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 ; Sequence 31, Application US/08485324
 ; Patent No. 6043093
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlstadter, Jacob
 ; TITLE OF INVENTION: SELECTION METHODS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris, & Safford
 ADDRESSEE: c/o Barry Evans
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,324
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/235,437
 FILING DATE: 29-APR-1994
 APPLICATION NUMBER: US 07/852,412
 FILING DATE: 16-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Evans, Barry
 REGISTRATION NUMBER: 22,802
 REFERENCE/DOCKET NUMBER: 370132-2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-485-324-31

Query Match 100.0%; Score 122; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
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 ; Patent No. 6066499
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlstadter, Jacob
 ; TITLE OF INVENTION: SELECTION METHODS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Curtis, Morris, & Safford
 ; ADDRESSEE: c/o Barry Evans
 ; STREET: 530 Fifth Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/447,506
 ; FILING DATE: 23-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/235,437
 ; FILING DATE: 29-APR-1994

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; APPLICATION NUMBER: US 07/852,412
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: Evans, Barry
;   REGISTRATION NUMBER: 22,802
;   REFERENCE/DOCKET NUMBER: 370132-2000
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 840-3333
;   TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 25 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
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Query Match      100.0%; Score 122; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Title: SEQ1

Perfect score: 122

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 250 summaries

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Published Applications AA:*

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- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	101	82.8	21	14 US-10-178-488-25	Sequence 25, Appl
5	99	81.1	20	9 US-09-813-659-3	Sequence 3, Appl
6	99	81.1	20	15 US-10-283-610A-3	Sequence 3, Appl
7	97	79.5	20	10 US-09-827-345-24	Sequence 24, Appl
8	95	77.9	20	14 US-10-311-111-1	Sequence 1, Appl
9	95	77.9	20	16 US-10-398-932-1	Sequence 1, Appl
10	82	67.2	18	14 US-10-062-710-45	Sequence 45, Appl
11	77	63.1	15	9 US-09-810-310-15	Sequence 15, Appl
12	77	63.1	15	9 US-09-810-310-24	Sequence 24, Appl
13	77	63.1	15	9 US-09-989-621-8	Sequence 8, Appl

14	77	63.1	15	10	US-09-827-688-9	Sequence 9, Appl
15	77	63.1	15	10	US-09-077-439A-3	Sequence 3, Appl
16	77	63.1	15	14	US-10-133-210-246	Sequence 246, App
17	77	63.1	15	14	US-10-133-210-262	Sequence 262, App
18	77	63.1	15	14	US-10-147-910-6	Sequence 6, Appl
19	77	63.1	15	17	US-10-787-880-2	Sequence 2, Appl
20	77	63.1	16	14	US-10-062-710-44	Sequence 44, Appl
21	76	62.3	23	17	US-10-621-675-154	Sequence 154, App
22	75	61.5	15	17	US-10-622-003-6	Sequence 6, Appl
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24	72	59.0	15	14	US-10-239-313A-186	Sequence 186, App
25	72	59.0	22	15	US-10-373-592-113	Sequence 113, App
26	71	58.2	22	15	US-10-373-592-112	Sequence 112, App
27	71	58.2	22	15	US-10-373-592-114	Sequence 114, App
28	71	58.2	24	17	US-10-628-004-12	Sequence 12, Appl
29	68	55.7	13	14	US-10-239-313A-536	Sequence 536, App
30	68	55.7	24	17	US-10-621-675-7	Sequence 7, Appl
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34	66	54.1	15	10	US-09-993-307-21	Sequence 21, Appl
35	65	53.3	17	15	US-10-360-647A-1	Sequence 1, Appl
36	65	53.3	17	17	US-10-613-018-1	Sequence 1, Appl
37	65	53.3	21	17	US-10-613-018-22	Sequence 22, Appl
38	65	53.3	21	17	US-10-613-018-40	Sequence 40, Appl
39	63	51.6	12	14	US-10-239-313A-535	Sequence 535, App
40	63	51.6	19	14	US-10-178-488-24	Sequence 24, Appl
41	62	50.8	13	14	US-10-311-111-3	Sequence 3, Appl
42	62	50.8	13	16	US-10-398-932-3	Sequence 3, Appl
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44	60	49.2	23	17	US-10-621-675-156	Sequence 156, App
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48	59	48.4	19	15	US-10-429-979-7	Sequence 7, Appl
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51	58	47.5	22	15	US-10-373-592-111	Sequence 111, App
52	58	47.5	23	17	US-10-621-675-158	Sequence 158, App
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63	54	44.3	19	14	US-10-059-271-33	Sequence 33, Appl
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65	53	43.4	22	15	US-10-373-592-104	Sequence 104, App
66	52	42.6	10	9	US-09-858-349-3	Sequence 3, Appl
67	52	42.6	10	9	US-09-810-310-16	Sequence 16, Appl
68	52	42.6	10	9	US-09-820-484-8	Sequence 8, Appl
69	52	42.6	10	9	US-09-087-513-7	Sequence 7, Appl
70	52	42.6	10	9	US-09-087-513-13	Sequence 13, Appl
71	52	42.6	10	10	US-09-997-848A-16	Sequence 16, Appl
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73	52	42.6	10	14	US-10-113-085-7	Sequence 7, Appl
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76	52	42.6	10	14	US-10-079-167-51	Sequence 51, Appl
77	52	42.6	10	14	US-10-079-167-68	Sequence 68, Appl
78	52	42.6	10	14	US-10-340-275-8	Sequence 8, Appl
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81	52	42.6	10	14	US-10-210-148-113	Sequence 113, App
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87	52	42.6	10	15	US-10-367-594-109	Sequence 109, App	160	44	36.1	13	15	US-10-373-592-118	Sequence 118, App
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89	52	42.6	10	15	US-10-367-658-109	Sequence 108, App	162	44	36.1	15	9	US-09-810-310-25	Sequence 25, Appl
90	52	42.6	10	15	US-10-367-668-109	Sequence 109, App	163	44	36.1	15	10	US-09-964-201A-2	Sequence 2, Appli
91	52	42.6	10	16	US-10-367-674-109	Sequence 109, App	164	44	36.1	15	14	US-10-041-414-39	Sequence 39, Appl
92	52	42.6	10	16	US-10-653-624-51	Sequence 51, Appl	165	44	36.1	15	15	US-10-338-592-12	Sequence 12, Appl
93	52	42.6	10	16	US-10-653-624-68	Sequence 68, Appl	166	44	36.1	15	15	US-10-369-121-37	Sequence 37, Appl
94	52	42.6	10	16	US-10-653-624-68	Sequence 68, Appl	167	44	36.1	15	16	US-10-681-389-2	Sequence 2, Appli
95	52	42.6	10	16	US-10-777-053-138	Sequence 138, App	168	44	36.1	15	16	US-10-681-388-2	Sequence 2, Appli
96	52	42.6	10	16	US-10-777-053-533	Sequence 533, App	169	44	36.1	15	16	US-10-753-339-50	Sequence 50, Appl
97	52	42.6	10	16	US-10-416-262B-8	Sequence 8, Appli	170	44	36.1	15	17	US-10-622-003-5	Sequence 5, Appli
98	52	42.6	10	16	US-10-833-439-51	Sequence 51, Appl	171	44	36.1	16	14	US-10-062-710-161	Sequence 161, App
99	52	42.6	10	16	US-10-833-439-68	Sequence 68, Appl	172	43	35.2	9	16	US-10-777-053-131	Sequence 131, App
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103	52	42.6	10	17	US-10-887-230-55	Sequence 55, Appl	176	43	35.2	14	16	US-10-654-200-42	Sequence 42, Appl
104	52	42.6	11	14	US-10-062-710-163	Sequence 32, App	177	43	35.2	14	16	US-10-654-200-89	Sequence 89, Appl
105	51	41.8	18	14	US-10-059-271-32	Sequence 24, Appl	178	43	35.2	15	9	US-09-810-310-30	Sequence 30, Appl
106	50	41.0	16	14	US-10-059-271-24	Sequence 2, Appli	179	43	35.2	15	16	US-10-654-200-87	Sequence 87, Appl
107	50	41.0	16	17	US-10-613-018-2	Sequence 36, Appl	180	43	35.2	21	16	US-10-654-200-88	Sequence 88, Appl
108	50	41.0	17	14	US-10-059-271-36	Sequence 13, Appl	181	42	34.4	15	17	US-10-622-003-7	Sequence 7, Appli
109	50	41.0	18	14	US-10-059-271-13	Sequence 35, Appl	182	42	34.4	18	14	US-10-053-271-14	Sequence 14, Appl
110	50	41.0	18	14	US-10-059-271-35	Sequence 35, Appl	183	42	34.4	18	15	US-10-469-256-13	Sequence 13, Appl
111	50	41.0	19	14	US-10-059-271-19	Sequence 19, Appl	184	42	34.4	22	15	US-10-373-592-117	Sequence 117, App
112	50	41.0	23	17	US-10-621-675-157	Sequence 157, App	185	41	33.6	9	10	US-09-997-848A-18	Sequence 18, Appl
113	50	41.0	23	17	US-10-621-675-114	Sequence 114, App	186	41	33.6	9	16	US-10-777-053-139	Sequence 139, App
114	49.5	40.6	16	15	US-10-360-647A-2	Sequence 2, Appli	187	41	33.6	15	17	US-10-622-003-2	Sequence 2, Appli
115	49	40.2	15	17	US-10-622-003-4	Sequence 4, Appli	188	41	33.6	15	17	US-10-622-003-15	Sequence 15, Appl
116	49	40.2	17	10	US-09-964-201A-3	Sequence 3, Appli	189	41	33.6	21	15	US-10-622-003-16	Sequence 16, Appl
117	49	40.2	17	16	US-10-681-389-3	Sequence 3, Appli	190	41	33.6	21	15	US-10-373-592-103	Sequence 103, App
118	49	40.2	17	16	US-10-681-388-3	Sequence 3, Appli	191	40	32.8	10	15	US-10-338-592-10	Sequence 10, Appl
119	49	40.2	19	14	US-10-178-488-23	Sequence 23, Appl	192	40	32.8	12	15	US-10-431-596-79	Sequence 79, Appl
120	49	40.2	20	15	US-10-338-592-13	Sequence 13, Appl	193	40	32.8	13	10	US-09-956-940-52	Sequence 52, Appl
121	49	40.2	24	10	US-09-956-940-21	Sequence 21, App	194	40	32.8	17	10	US-09-930-915A-6	Sequence 6, Appli
122	48	39.3	9	14	US-10-239-313A-532	Sequence 1, Appli	195	40	32.8	17	14	US-10-082-014-12	Sequence 12, Appl
123	48	39.3	9	16	US-10-777-053-146	Sequence 146, App	196	40	32.8	17	16	US-10-806-006-6	Sequence 6, Appli
124	48	39.3	18	14	US-10-059-271-25	Sequence 25, Appl	197	40	32.8	17	16	US-10-677-074-12	Sequence 12, Appl
125	48	39.3	18	14	US-10-059-271-27	Sequence 27, Appl	198	40	32.8	17	16	US-10-805-913-6	Sequence 6, Appli
126	48	39.3	18	14	US-09-825-886-30	Sequence 30, Appl	199	40	32.0	12	10	US-09-964-201A-16	Sequence 16, Appl
127	47	38.5	9	17	US-10-494-161-17	Sequence 17, Appl	200	39	32.0	12	10	US-10-431-596-81	Sequence 81, Appl
128	47	38.5	10	15	US-09-956-940-51	Sequence 51, Appl	201	39	32.0	12	15	US-10-681-389-16	Sequence 16, Appl
129	47	38.5	15	15	US-10-360-647A-18	Sequence 18, Appl	202	39	32.0	12	16	US-10-681-388-16	Sequence 16, Appl
130	46	37.7	15	17	US-10-622-003-11	Sequence 11, Appl	203	39	32.0	12	16	US-09-810-310-32	Sequence 32, Appl
131	46	37.7	15	17	US-10-613-018-23	Sequence 23, Appl	204	39	32.0	15	9	US-10-442-909-42	Sequence 42, Appl
132	46	37.7	18	17	US-10-613-018-41	Sequence 41, Appl	205	39	32.0	15	17	US-10-622-003-10	Sequence 10, Appl
133	46	37.7	18	17	US-10-613-018-42	Sequence 42, Appl	206	39	32.0	16	14	US-10-016-986-141	Sequence 141, App
134	46	37.7	23	17	US-10-621-675-163	Sequence 163, App	207	39	32.0	16	14	US-10-655-702-3	Sequence 3, Appli
135	46	37.7	25	17	US-10-621-675-17	Sequence 17, App	208	38	31.1	10	9	US-09-810-310-17	Sequence 17, Appl
136	46	37.7	25	17	US-10-373-592-109	Sequence 109, App	209	38	31.1	10	9	US-09-873-459A-3	Sequence 3, Appli
137	45.5	37.3	24	15	US-10-079-167-52	Sequence 52, Appl	210	38	31.1	12	9	US-10-016-986-48	Sequence 48, Appl
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139	45	36.9	9	14	US-10-367-580-115	Sequence 115, App	212	38	31.1	12	14	US-10-654-200-41	Sequence 41, Appl
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141	45	36.9	9	15	US-10-367-594-115	Sequence 115, App	214	38	31.1	14	16	US-10-654-200-90	Sequence 90, Appl
142	45	36.9	9	15	US-10-367-654-115	Sequence 115, App	215	38	31.1	15	16	US-10-059-271-26	Sequence 26, Appl
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145	45	36.9	9	16	US-10-367-674-115	Sequence 115, App	218	37	30.3	13	14	US-10-059-271-20	Sequence 20, Appl
146	45	36.9	9	16	US-10-653-624-52	Sequence 52, App	219	37	30.3	17	14	US-10-059-271-20	Sequence 20, Appl
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148	45	36.9	9	16	US-10-833-745-52	Sequence 52, Appl	221	36	29.5	9	16	US-10-777-053-305	Sequence 305, App
149	45	36.9	9	16	US-10-833-744-52	Sequence 52, Appl	222	36	29.5	10	9	US-09-810-310-23	Sequence 23, Appl
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151	45	36.9	15	15	US-10-338-592-11	Sequence 11, Appl	224	36	29.5	10	9	US-09-087-513-18	Sequence 18, Appl
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153	45	36.9	15	17	US-10-622-003-13	Sequence 13, Appl	226	36	29.5	15	9	US-10-080-608A-71	Sequence 71, Appl
154	45	36.9	20	17	US-10-628-004-9	Sequence 9, Appli	227	36	29.5	24	14	US-10-371-067-2	Sequence 2, Appli
155	45	36.9	20	17	US-10-628-004-10	Sequence 10, Appl	228	36	29.5	24	15	US-09-997-848A-17	Sequence 17, Appl
156	45	36.9	24	15	US-10-373-592-110	Sequence 110, App	229	35.5	29.1	9	10	US-09-775-805-6	Sequence 6, Appli
157	45	36.9	12	15	US-10-431-596-78	Sequence 78, Appl	230	35	28.7	10	9	US-10-200-708-627	Sequence 627, App
158	44	36.1	13	14	US-10-213-742-1	Sequence 1, Appli	231	35	28.7	10	14		
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 236 Sequence 6, Appl
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 238 Sequence 245, App
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 240 Sequence 5, Appl
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 248 Sequence 60, Appl
 249 Sequence 18, Appl
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ALIGNMENTS

RESULT 1
 US-10-621-675-160
 ; Sequence 160, Application US/10621675
 ; Publication No. US20050049398A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Leys, Robert
 ; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
 ; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
 ; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
 ; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
 ; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
 ; TITLE OF INVENTION: CONTAINING THEM
 ; FILE REFERENCE: 2752-11
 ; CURRENT APPLICATION NUMBER: US/10/621,675
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: US/09/576,824A
 ; PRIOR APPLICATION NUMBER: 08/723,425
 ; PRIOR FILING DATE: 1996-09-30
 ; PRIOR APPLICATION NUMBER: 09/146,028
 ; PRIOR FILING DATE: 1993-11-22
 ; PRIOR APPLICATION NUMBER: PCT/EP93/00517
 ; PRIOR FILING DATE: 1993-03-08
 ; PRIOR APPLICATION NUMBER: EP 92400598.6
 ; PRIOR FILING DATE: 1992-03-06
 ; NUMBER OF SEQ ID NOS: 600
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 160
 ; LENGTH: 24
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-621-675-160

Query Match 100.0%; Score 122; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.8e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 NNTKRSIRIQGPGRAFVTIGKIG 24

RESULT 2
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 ; Sequence 13, Application US/10876343A
 ; Publication No. US20050106560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlstadter, Jacob N
 ; TITLE OF INVENTION: Selection Methods
 ; FILE REFERENCE: 100405-02121
 ; CURRENT APPLICATION NUMBER: US/10/876,343A

; CURRENT FILING DATE: 2004-06-23
 ; PRIOR APPLICATION NUMBER: US 09/573,830
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 6,087,177
 ; PRIOR FILING DATE: 1994-04-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 13
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic HIV gp120, variable region 3, aa 271-295
 US-10-876-343A-13

Query Match 100.0%; Score 122; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;
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 Db 1 NNTKRSIRIQGPGRAFVTIGKIG 24

RESULT 3
 US-10-876-343A-31
 ; Sequence 31, Application US/10876343A
 ; Publication No. US20050106560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlstadter, Jacob N
 ; TITLE OF INVENTION: Selection Methods
 ; FILE REFERENCE: 100405-02121
 ; CURRENT APPLICATION NUMBER: US/10/876,343A
 ; CURRENT FILING DATE: 2004-06-23
 ; PRIOR APPLICATION NUMBER: US 09/573,830
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 6,087,177
 ; PRIOR FILING DATE: 1994-04-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 31
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 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic HIV gp120, variable region 3, aa 271-295
 US-10-876-343A-31

Query Match 100.0%; Score 122; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 NNTKRSIRIQGPGRAFVTIGKIG 24

RESULT 4
 US-10-178-488-25
 ; Sequence 25, Application US/10178488
 ; Publication No. US20030165535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rovinski, Benjamin
 ; APPLICANT: Cao, Shi-Xian
 ; APPLICANT: Yao, Fei-Long
 ; APPLICANT: Persson, Roy
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: RETROVIRUS-LIKE PARTICLES MADE NON-INFECTIONOUS BY A
 ; TITLE OF INVENTION: PLURALITY OF MUTATIONS
 ; FILE REFERENCE: 1038-1238 MIS
 ; CURRENT APPLICATION NUMBER: US/10/178,488
 ; CURRENT FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: 09/258,128

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; PRIOR FILING DATE: 1993-02-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Artificial
US-10-178-488-25

Query Match      82.8%; Score 101; DB 14; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 NTRKRIRIQRGPGRAFTVIGK 21
    |||||

RESULT 5
US-09-813-659-3
; Sequence 3, Application US/09813659
; Patent No. US20020012989A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-3

Query Match      81.1%; Score 99; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKSIRIQRGPGRAFTVIGKI 23
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Db 1 RKSIRIQRGPGRAFTVIGKI 20
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RESULT 6
US-10-283-610A-3
; Sequence 3, Application US/10283610A
; Publication No. US20030219876A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; FILE REFERENCE: 30436.18USD3
; CURRENT APPLICATION NUMBER: US/10/283,610A
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-610A-3

Query Match      81.1%; Score 99; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKSIRIQRGPGRAFTVIGKI 23
    |||||
Db 1 RKSIRIQRGPGRAFTVIGKI 20
    |||||

RESULT 7
US-09-827-345-24
; Sequence 345-24, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CONTEL, CAROLE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 063691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCI/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-827-345-24

Query Match      79.5%; Score 97; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 NNTRKSIRIQRGPGRAFTV 20
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RESULT 8
US-10-311-111-1
; Sequence 1, Application US/10311111
; Publication No. US20030121065A1
; GENERAL INFORMATION:
; APPLICANT: SHIBA, KIYOTAKA
; TITLE OF INVENTION: MULTIFUNCTIONAL BASE SEQUENCE AND ARTIFICIAL GENE CONTAINING THE
; FILE REFERENCE: 4439-4004
; CURRENT APPLICATION NUMBER: US/10/311,111
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: JP 2000-180997
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide
US-10-311-111-1
Query Match 77.9%; Score 95; DB 14; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RKSIRIQRGPGRAFTVIGKI 23
Db 1 RKSIRIQRGPGRTFTVIGKI 20

RESULT 9
US-10-398-932-1
; Sequence 1, Application US/10398932
; Publication No. US20040171803A1
; GENERAL INFORMATION:
; APPLICANT: SHIBA, KIYOTAKA
; APPLICANT: OHNO, TSUNEYA
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH ENRICHED IMMUNOGEN
; TITLE OF INVENTION: OF EPITOPE
; FILE REFERENCE: 024918-0103
; CURRENT APPLICATION NUMBER: US/10/398,932
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08893
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: JP. 2000/314288
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetically Designed
; OTHER INFORMATION: Peptide
US-10-398-932-1
Query Match 77.9%; Score 95; DB 16; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RKSIRIQRGPGRAFTVIGKI 23
Db 1 RKSIRIQRGPGRTFTVIGKI 20

RESULT 10
US-10-062-710-45
; Sequence 45, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:

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; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-45
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Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IQRGPGRAFTVIGKI 24
Db 2 IQRGPGRAFTVIGKI 17

RESULT 11
US-09-810-310-15
; Sequence 15, Application US/09810310
; Patent No. US2002004948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-15
Query Match 63.1%; Score 77; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RIQRGPGRAFTVIGK 22
Db 1 RIQRGPGRAFTVIGK 15

RESULT 12
US-09-810-310-24
; Sequence 24, Application US/09810310
; Patent No. US2002004948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS

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; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-24

Query Match      63.1%; Score 77; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 RIQGGGCGRAFTVIGK 22
Db      1 RIQGGGCGRAFTVIGK 15

RESULT 13
US-09-989-621-8
; Sequence 8, Application US/09989621
; Patent No. US20020151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Youn
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/989,621
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HIV
US-09-989-621-8

Query Match      63.1%; Score 77; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 RIQGGGCGRAFTVIGK 22
Db      1 RIQGGGCGRAFTVIGK 15

RESULT 14
US-09-827-688-9
; Sequence 9, Application US/09827688
; Publication No. US20030165476A1
; GENERAL INFORMATION:
; APPLICANT: ORSON, FRANK
; APPLICANT: KINSEY, BERMA
; APPLICANT: BHOGAL, BALRIR
; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P01949US1/10004014
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; CURRENT APPLICATION NUMBER: US/09/827,688
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,680
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HIV p18
US-09-827-688-9

Query Match      63.1%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 RIQGGGCGRAFTVIGK 22
Db      1 RIQGGGCGRAFTVIGK 15

RESULT 15
US-09-077-439A-3
; Sequence 3, Application US/09077439A
; Publication No. US20030202989A1
; GENERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Blanke, Steven R.
; APPLICANT: Milne, Jill C.
; APPLICANT: Benson, Ericka L.
; APPLICANT: Ballard, Jimmy D.
; APPLICANT: Starnbach, Michael N.
; TITLE OF INVENTION: Use of Toxin Peptides and/or Affinity
; TITLE OF INVENTION: Handles for Delivering Compounds into Cells
; FILE REFERENCE: 00246/187002
; CURRENT APPLICATION NUMBER: US/09/077,439A
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US96/20463
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: US 60/019,275
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 60/008,518
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-077-439A-3

Query Match      63.1%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 RIQGGGCGRAFTVIGK 22
Db      1 RIQGGGCGRAFTVIGK 15

Search completed: June 3, 2005, 03:24:18
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Syncytium
(plural,
syncytia)

Multi-nucleate cells formed by the fusion of neighboring cells. Syncytia may form due to the expression of a viral fusion protein during viral replication.

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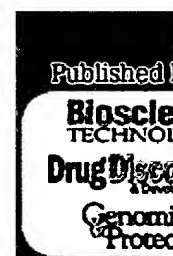
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OM protein - protein search, using sw model

Run on: June 3, 2005, 03:02:32 ; Search time 156 Seconds
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59,502 Million cell updates/sec

Title: SEQ1

Perfect score: 122

Sequence: 1 nntksirigrgpgrafvtigkig 24

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 768190

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 250 summaries

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2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	122	100.0	24	2 AAR06211	Aar06211 Immunosup
2	122	100.0	24	2 AAR07018	Aar07018 Residues
3	122	100.0	24	2 AAR26565	Aar26565 Sequence
4	122	100.0	24	2 AAR29233	Aar29233 Heterocon
5	122	100.0	24	2 AAR28870	Aar28870 HIV gp120
6	122	100.0	24	2 AAR34406	Aar34406 Sequence
7	122	100.0	24	2 AAR38165	Aar38165 V3 loop p
8	122	100.0	24	2 AAR22581	Aar22581 HIV LBL b
9	122	100.0	24	3 AAB15873	Aab15873 Human che
10	122	100.0	24	4 AAB68602	Aab68602 HIV gp120
11	122	100.0	25	1 AAP90281	Aap90281 Peptide 1
12	122	100.0	25	2 AAR08276	Aar08276 HIV pepti
13	122	100.0	25	2 AAR31276	Aar31276 HIV princ
14	122	100.0	25	2 AAR30031	Aar30031 HIV princ
15	122	100.0	25	2 AAR26712	Aar26712 HIV-PND-p
16	122	100.0	25	2 AAR33222	Aar33222 HIV gp120
17	122	100.0	25	2 AAR41336	Aar41336 HIV gp120
18	122	100.0	25	2 AAR41330	Aar41330 HIV gp120
19	120	98.4	25	2 AAR04427	Aar04427 Human imm
20	118	96.7	24	2 AAR22583	Aar22583 HIV LBL b
21	116	95.1	23	2 AAR04502	Aar04502 CpD. elic
22	116	95.1	24	2 AAR3190	Aar3190 Sequence
23	116	95.1	24	2 AAR67414	Aar67414 HIV-1 pep
24	116	95.1	24	2 AAR98904	Aar98904 HIV-1 vac
25	116	95.1	24	2 AAR39769	Aar39769 HIV1 chim

26	116	95.1	25	2 AAR15058	Aar15058 HIV-1 amp
27	116	95.1	25	2 AAR36587	Aar36587 Virus neu
28	113	92.6	25	2 AAR04475	Aar04475 Human imm
29	112	91.8	25	2 AAR87618	Aar87618 Epitope o
30	110	90.2	22	2 AAR42153	Aar42153 gp120 V3
31	110	90.2	22	2 AAR07392	Aar07392 HIV-1 str
32	110	90.2	22	2 AAY07488	Aay07488 HIV-1 str
33	107	87.7	25	2 AAR13120	Aar13120 Binding s
34	107	87.7	25	2 AAY72819	Aay72819 HIV-1 gp1
35	106	86.9	22	3 AAY85137	Aay85137 HIV-1 III
36	101	82.8	20	2 AAR76842	Aar76842 Fusion im
37	101	82.8	21	2 AAR04060	Aar04060 Epitope c
38	101	82.8	21	2 AAR93073	Aar93073 Antigenic
39	101	82.8	21	2 AAY75478	Aay75478 HIV-1 str
40	101	82.8	21	2 AAY16052	Aay16052 HIV-1 iso
41	101	82.8	21	2 AAR85568	Aar85568 Human imm
42	101	82.8	21	4 AAR08699	Aar08699 Retroviri
43	101	82.8	22	2 AAR57470	Aar57470 HIV BRU V
44	101	82.8	24	5 AAE20149	Aae20149 Human imm
45	101	82.8	25	2 AAR63820	Aar63820 HIV-1 gp1
46	100	82.0	20	2 AAW54930	Aaw54930 HIV gp120
47	100	82.0	20	8 ADR18886	Adr18886 HIV-1 V3-
48	100	82.0	23	4 AAB66704	Aab66704 HIV-1 III
49	99	81.1	20	2 AAR60203	Aar60203 HIV gp110
50	97	79.5	25	1 AAP90283	Aap90283 Peptide 1
51	97	79.5	25	2 AAR04479	Aar04479 Human imm
52	96	78.7	20	2 AAR68680	Aar68680 B cell ep
53	96	78.7	20	2 AAW25898	Aaw25898 HIV-1 str
54	96	78.7	20	2 AAW25850	Aaw25850 HIV-1 str
55	96	78.7	20	2 AAW67366	Aaw67366 HIV-1 str
56	96	78.7	20	2 AAY99974	Aay99974 HIV-1 vac
57	96	78.7	20	2 AAY39699	Aay39699 HIV1 chim
58	96	78.7	20	6 AAB57070	Aab57070 HIV gp120
59	95	77.9	20	2 AAR25471	Aar25471 V3 loop s
60	95	77.9	20	5 ABB05775	Abb05775 HIV gp120
61	95	77.9	20	5 AAO15657	Aao15657 Strong im
62	95	77.9	25	4 AAE09522	Aae09522 Human imm
63	93	76.2	23	2 AAR04476	Aar04476 Human imm
64	91	74.6	21	2 AAW34475	Aaw34475 Acceptor
65	91	74.6	22	6 ABU07537	Abu07537 Human N-a
66	91	74.6	24	2 AAR63821	Aar63821 HIV-1 gp1
67	91	74.6	25	1 AAR82464	Aar82464 Peptide c
68	90	73.8	18	2 AAR44190	Aar44190 gp120 V3
69	90	73.8	18	2 AAR58548	Aar58548 HIV-1 iso
70	90	73.8	18	8 ADR18878	Adr18878 HIV-1 V3-
71	90	73.8	24	2 AAR44191	Aar44191 gp120 V3
72	88	72.1	18	2 AAY22593	Aay22593 HIV putat
73	87	71.3	18	2 AAR31277	Aar31277 HIV princ
74	87	71.3	18	2 AAR30032	Aar30032 HIV princ
75	87	71.3	18	2 AAR26713	Aar26713 HIV-PND-p
76	86.5	70.9	21	2 AAR27465	Aar27465 V3 peptid
77	86.5	70.9	21	2 AAR31219	Aar31219 V3 peptid
78	86	70.5	21	2 AAR68645	Aar68645 VP hybrid
79	86	70.5	21	2 AAW25815	Aaw25815 Chimaeric
80	86	70.5	21	2 AAW67331	Aaw67331 HIV-1 pep
81	86	70.5	21	2 AAW99939	Aaw99939 HIV-1 vac
82	86	70.5	21	2 AAY39690	Aay39690 HIV1 gag
83	85	69.7	17	1 AAP95348	Aap95348 Variable
84	85	69.7	17	2 AAR29241	Aar29241 V3 loop r
85	85	69.7	17	2 AAR32407	Aar32407 Sequence
86	85	69.7	17	2 AAR68664	Aar68664 T cell ep
87	85	69.7	17	2 AAW25834	Aaw25834 HIV B-cel
88	85	69.7	17	2 AAW67350	Aaw67350 HIV-1 str
89	85	69.7	17	2 AAW99958	Aaw99958 HIV-1 vac
90	85	69.7	17	2 AAY39756	Aay39756 HIV1 chim
91	85	69.7	17	8 ADR18895	Adr18895 HIV-1 V3
92	82	67.2	17	7 ADNI4075	Adni4075 HIV helpe
93	82	67.2	24	2 AAR74608	Aar74608 HIV-1 gp1
94	81	66.4	16	2 AAR24939	Aar24939 HIV pepti
95	81	66.4	16	2 AAW68326	Aaw68326 MHC bindi
96	81	66.4	16	3 AAY68203	Aay68203 Altered M
97	81	66.4	16	3 AAY52857	Aay52857 Altered M
98	81	66.4	16	4 AAB58618	Aab58618 Altered M

08/869,386

Fri Jun 3 06:53:20 2005

99	81	66.4	17	1	AAP95349	Variable	172	73	59.8	15	2	AAR66430	Aar66430	HIV-1 III
100	81	66.4	17	2	AAV40414	Lipopepti	173	73	59.8	15	2	AAR66424	Aar66424	HIV-1 III
101	81	66.4	18	4	ABB83113	Lipopepti	174	73	59.8	16	2	AAW76837	Fusion im	
102	81	66.4	21	3	ABJ5012	Peptide P	175	73	59.8	19	2	AAR60663	HTLV-LAV-	
103	80	65.6	16	2	AAR33236	HIV-IIIB	176	73	59.8	19	2	AAR60655	HTLV-IIIB	
104	80	65.6	17	2	AAR76848	Fusion im	177	73	59.8	19	2	AAR85359	SP-10 reg	
105	80	65.6	18	2	AAR38526	Cyclic HI	178	73	59.8	19	2	AAW16501	SP-10 LAV	
106	80	65.6	18	2	AAW03404	HIV princ	179	73	59.8	19	2	AAW16510	SP-10 III	
107	79	64.8	16	8	ADR18865	V3-IIIB b	180	73	59.8	19	6	ABU07506	HIV glyco	
108	79	64.8	22	2	AAV22589	HIV LDL b	181	73	59.8	19	2	AAW76895	Synthetic	
109	78	63.9	15	1	AAP90221	Antigenic	182	73	59.8	20	2	AAW60678	Fusion im	
110	78	63.9	19	2	AAW42127	CD4+ T-ly	183	73	59.8	20	2	AAW73258	SP-10 lik	
111	78	63.9	20	2	AAW54328	HIV gpl20	184	73	59.8	20	2	AAW42156	SP-120 V3	
112	78	63.9	21	2	AAW79180	Fusion im	185	73	59.8	22	2	AAW76895	Sequence	
113	78	63.9	21	1	AAP76901	Fusion im	186	73	59.8	22	2	AAW07495	HIV-1 str	
114	77	63.1	15	1	AAP82095	Env-K1 pe	187	73	59.8	24	2	AAW04467	Human imm	
115	77	63.1	15	1	AAP91228	Peptide c	188	73	59.8	24	2	AAW07490	HIV-1 str	
116	77	63.1	15	2	AAR21343	HIV-1 gpl	189	73	59.8	25	2	AAR41066	HIV-1 par	
117	77	63.1	15	2	AAR38187	V3 loop p	190	72	59.0	14	2	AAW66416	HIV-1 III	
118	77	63.1	15	2	AAR32207	Sequence	191	72	59.0	14	2	AAW76896	Fusion im	
119	77	63.1	15	2	AAR51619	V3 loop r	192	72	59.0	15	2	AAR33460	Sequence	
120	77	63.1	15	2	AAR74603	HIV-1 var	193	72	59.0	15	2	AAR66427	HIV-1 III	
121	77	63.1	15	2	AAR66414	HIV-1 III	194	72	59.0	15	2	AAR66428	HIV-1 III	
122	77	63.1	15	2	AAR68789	Cytotoxic	195	72	59.0	15	2	AAR66426	HIV-1 III	
123	77	63.1	15	2	AAR05535	HIV-1 gpl	196	72	59.0	15	2	AAR76897	Fusion im	
124	77	63.1	15	2	AAR92033	Hydrophil	197	72	59.0	15	3	AAW85592	HIV pepti	
125	77	63.1	15	2	AAR07931	Gp120 pep	198	72	59.0	15	3	AAW99083	Vaccine r	
126	77	63.1	15	2	AAR92007	HIV-1 V3	199	72	59.0	15	4	AAW99083	Vaccine r	
127	77	63.1	15	2	AAW24219	CD4+ T-ly	200	72	59.0	20	8	ADJ18892	HIV-1 V3	
128	77	63.1	15	2	AAW10348	HIV epit	201	72	59.0	22	8	ADJ56924	HIV-1 env	
129	77	63.1	15	2	AAW22031	Antigenic	202	71	58.2	22	8	ADJ58171	Novel ant	
130	77	63.1	15	2	AAW39275	HIV-1 syn	203	71	58.2	15	2	AAR66420	HIV-1 III	
131	77	63.1	15	2	AAW40316	HIV-1 III	204	71	58.2	15	2	AAR66429	HIV-1 III	
132	77	63.1	15	2	AAW76898	Fusion im	205	71	58.2	15	2	AAR66423	HIV-1 III	
133	77	63.1	15	2	AAW54929	Sequence	206	71	58.2	15	2	AAR66422	HIV-1 III	
134	77	63.1	15	2	AAW06896	HIV pep	207	71	58.2	22	8	ADJ56925	HIV-1 env	
135	77	63.1	15	2	AAW24466	HIV prote	208	71	58.2	22	8	ADJ56923	HIV-1 env	
136	77	63.1	15	2	AAW25189	HIV V3 pe	209	71	58.2	22	8	ADR58170	Novel ant	
137	77	63.1	15	2	AAW05356	HIV-1 CLU	210	71	58.2	22	8	ADR58172	Novel ant	
138	77	63.1	15	2	AAW72821	HIV-1 gpl	211	71	58.2	23	2	AAW19022	HIV envel	
139	77	63.1	15	2	AAW87620	Epitope o	212	71	58.2	23	2	AAW07916	Gp120 pep	
140	77	63.1	15	2	AAW04680	HIV-1 gpl	213	71	58.2	24	2	Aaw23864	HIV-1 str	
141	77	63.1	15	2	AAW83916	HIV-1 env	214	71	58.2	24	2	ABp22870	HIV-1 gpl	
142	77	63.1	15	3	AAV66439	HLA-A2-bi	215	71	58.2	25	2	AAW57471	HIV MN V3	
143	77	63.1	15	3	AAV66455	HLA-A3-bi	216	71	58.2	18	3	AAW57471	Glycoprot	
144	77	63.1	15	3	AAV66455	HLA-A3-bi	217	70	57.4	14	1	AAW96191	HIV-1 env	
145	77	63.1	15	3	AAV85591	HIV relat	218	70	57.4	18	1	AAW91793	Fusion im	
146	77	63.1	15	3	AAV15875	Human che	219	70	57.4	14	2	AAW76863	Fusion imm	
147	77	63.1	15	3	AAV22345	Virus rel	220	70	57.4	18	2	AAW63062	Human imm	
148	77	63.1	15	4	AAV92348	Virus rel	221	70	57.4	14	2	AAW45603	HIV-1 V3	
149	77	63.1	15	4	AAV68601	HIV gpl20	222	69	56.6	22	2	AAY04446	Peptide p	
150	77	63.1	15	5	AAE15743	Human imm	223	69	56.6	15	2	AAY04446	Peptide p	
151	77	63.1	15	5	AAU96031	HIV epit	224	68	55.7	24	2	AAR12179	HIV SP-10	
152	77	63.1	15	5	AAU97690	HIV CTL e	225	68	55.7	13	2	AAW22327	HIV-1 str	
153	77	63.1	15	5	ABG68654	HIV-1 P18	226	68	55.7	13	2	AAW62890	Peptide s	
154	77	63.1	15	5	ABG68663	HIV-1 P18	227	68	55.7	13	4	AAW99433	Vaccine r	
155	77	63.1	15	6	AAE35161	HIV CTL e	228	68	55.7	14	2	AAW66417	Peptide f	
156	77	63.1	15	7	ADN14074	HIV helpe	229	68	55.7	19	2	AAW4218	HIV-1 III	
157	77	63.1	15	8	ADR04041	Immune re	230	67	54.9	22	2	AAW42181	CD4+ T-ly	
158	77	63.1	17	2	AAW42057	Peptide C	231	67	54.9	22	2	AAW07500	HIV envel	
159	76	62.3	15	1	AAW95357	Variable	232	67	54.9	15	2	AAW32887	HIV envel	
160	76	62.3	15	2	AAW62166	HIV-1 gpl	233	66.5	54.5	16	2	AAW32887	HIV envel	
161	76	62.3	15	2	AAW62166	HIV-1 gpl	234	66	54.1	20	1	AAW83004	Peptide f	
162	75	61.5	15	2	AAW76846	Fusion im	235	66	54.1	13	2	AAW58602	Alkaline	
163	75	61.5	15	2	AAW76846	Fusion im	236	66	54.1	13	2	AAW58601	Alkaline	
164	75	61.5	15	8	ADP76013	Peptide e	237	66	54.1	13	2	AAW58602	Alkaline	
165	74.5	61.1	17	1	AAW95356	Variable	238	66	54.1	13	2	AAW58603	Alkaline	
166	74	60.7	15	2	AAW66419	HIV-1 III	239	66	54.1	16	2	AAW38249	Alkaline	
167	74	60.7	15	2	AAW36156	HIV-1 str	240	66	54.1	14	2	AAW54927	Alkaline	
168	74	60.7	15	5	AAW49356	HIV-1 iso	241	66	54.1	14	2	AAW54927	Alkaline	
169	74	60.7	19	2	AAW22329	Peptide s	242	66	54.1	14	2	AAW54927	Alkaline	
170	73	59.8	14	2	AAW62892	Fusion im	243	66	54.1	14	2	AAW99595	HIV-1 vac	
171							244	66	54.1	14	2	AAW99595	HIV-1 vac	

245 66 54.1 15 2 AAR40198 Sequence
 246 66 54.1 15 2 AAR60675 HTLV SP-1
 247 66 54.1 15 2 AAR58606 Alkaline
 248 66 54.1 15 2 AAR85382 HTLV-III
 249 66 54.1 15 2 AAR16525 SP-10 C r
 250 66 54.1 15 2 AAR73255 SP-10 C r

ALIGNMENTS

RESULT 1
 AAR06211
 ID AAR06211 standard; peptide; 24 AA.

XX AC AAR06211;
 DT 10-DEC-1990 (first entry)
 XX DE Immunosuppressant protease inhibitor.
 XX KW Organ transplant; autoimmune disease; allergy; aplastic anaemia;
 XX KW systemic erythematodes.
 XX OS Synthetic.
 XX PN JP02157229-A.
 XX PD 18-JUN-1990.
 XX PF 07-DEC-1988; 88JP-00310635.
 XX PR 07-DEC-1988; 88JP-00310635.
 XX PA (NITL) NITTO DENKO CORP.
 XX DR WPI; 1990-233739/31.
 XX PT Protease inhibiting peptide immuno-suppressant - used to suppress
 PT rejection reaction in organs transplantation.
 XX PS Claim 1; Page 181; 6pp; Japanese.
 XX CC Protease inhibitor may be used to suppress organ transplant rejection
 CC without serious side effects. It may also be used in prevention and
 CC therapy of allergy, aplastic anaemia and systemic erythematodes. See
 CC also AAR06212

XX SQ Sequence 24 AA;

Query Match 100.0%; Score 122; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 2.6e-10;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24

Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 2

AAR07018

ID AAR07018 standard; peptide; 24 AA.

XX AC AAR07018;

DT 24-OCT-2003 (revised)

DT 18-JAN-1991 (first entry)

XX DE Residues 301-324 of HIV gp 120 protein used in isolation of sulphated

XX DE polysaccharide by affinity chromatography.

XX KW HIV; AIDS; ARC; gp120; RP135.

XX PT

OS Human immunodeficiency virus 1.

XX CA2007258-A.

XX PD 11-JUL-1990.

XX PF 05-JAN-1990; 90CA-02007258.

XX PR 11-JAN-1989; 89US-00295856.

XX PR 05-JUL-1989; 89US-00375795.

XX PA (RICH) MERRELL DOW PHARM INC.

XX PI Cardin AD, Jackson RL;

XX DR WPI; 1990-290631/39.

XX PT Prepn. of anti-HIV sulphated polysaccharide - by affinity chromatography

XX PT using a resin-bound peptide corresp. to a HIV gp. 120 fragment.

XX PS Disclosure; Page ?; 34pp; English.

XX CC Anti-HIV sulphated polysaccharide (SPS) can prevent syncytium formation

XX CC in HIV infected C4 cells. SPS may be isolated by affinity chromatography

XX CC with the given resin bound peptide fragment RP135. (Updated on 24-OCT-

XX CC 2003 to standardise OS field)

XX SQ Sequence 24 AA;

Query Match 100.0%; Score 122; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 2.6e-10;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24

Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 3

AAR26565

ID AAR26565 standard; peptide; 24 AA.

XX AC AAR26565;

XX DT 24-OCT-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 28-JAN-1993 (first entry)

XX DE Sequence of peptide DB1 determined from the V3 principal neutralising

XX DE domain (PND) region of HIV-1 strain HTLV-III B.

XX KW Diagnostic; assay; detection; AIDS; human immunodeficiency virus.

XX OS Human immunodeficiency virus 1; strain HTLV-III B.

XX PN WO9213882-A1.

XX PD 20-AUG-1992.

XX PF 29-JAN-1992; 92WO-EP000187.

XX PR 30-JAN-1991; 91IT-MI000220.

XX PA (SUPE-) INST SUPERIORE DI SANITA.

XX PA (CNDR) CONSIGLIO NAZ DELLE RICERCHE.

XX PI De Rossi A, Paesti M, Mammano F, Panozzo M, Dettin M, Di Bello C;

XX PI Chieco-Bianchi L;

XX DR WPI; 1992-299983/36.

XX PT Synthetic peptide(s) which enhance infectivity of HIV-1 in cellular

XX PT cultures - are used for determining HIV-1 virus in blood and other

CC maleimidomethyl cyclohexanecarboxylate (SMCC) as a conjugating agent.
CC Viruses containing these or similar sequences may be recognised by the
CC heteroconjugate enzymes of the invention. The antibodies raised against
CC these sequences may be identified by standard epitope mapping techniques.
CC These antibodies are capable, even at low concentrations, of nearly
CC eliminating viral replication of different strains of HIV. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX SQ Sequence 24 AA;
Query Match 100.0%; Score 122; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNTKSIIRIQPGRAFTVIGKIG 24
DB 1 NNTKSIIRIQPGRAFTVIGKIG 24
RESULT 5
AAR26870
ID AAR26870 standard; peptide; 24 AA.
XX
AC AAR26870;
XX
AC AC
XX
DT 25-MAR-2003 (revised)
DT 20-MAY-1998 (first entry)
XX
DE HIV gp120 V3 region binding assay peptide IIIB.
XX
KW Human immunodeficiency virus; AIDS; anti-gp120 antibodies.
XX
OS Synthetic.
XX
PN 16-SEP-1992;
XX 92EP-00302064.
XX 1-MAR-1992;
XX 91US-00668266.
XX 14-MAR-1991;
XX 06-MAR-1992; 92US-00894766.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Chang-Yuil K;
XX
PI WPI; 1992-309988/38.
XX
DR Anti-idiotype antibodies and methods for their selection - useful as
XX vaccines for the prevention and treatment of HIV infection.
XX
PS Example; Page 9; 30pp; Japanese.
XX
XX The sequence is that of peptide IIIB, derived from the V3 region of HIV
XX gp120, it was used in binding assays for anti-gp120 antibodies. The anti-
XX gp120 antibodies are useful in vaccine formulations for the treatment or
XX prevention of HIV infection. See also AAR26867-R26873. (Updated on 25-MAR
XX -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 24 AA;
Query Match 100.0%; Score 122; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNTKSIIRIQPGRAFTVIGKIG 24
DB 1 NNTKSIIRIQPGRAFTVIGKIG 24
RESULT 6
AAR32406

PT biological materials.
PS Claim 1; Page 17; 3lpp; English.
XX
XX The principal neutralizing domain (PND) of HIV-1 corresp. to a 24- amino
XX acid sequence arranged in a loop determined by a disulfide bridge in the
XX third hypervariable region, V3, of the protein gp 120. The central
XX portion of the V3-PND contains a sequence which is highly conserved in
XX different HIV-1 isolated strains, whereas the amino acids flanking this
XX sequence are variable. The antigenic properties of V3 region are known to
XX be virus-specific; antibodies elicited by MN-derived peptide do not
XX neutralize HTLV-III B virus and vice-versa. (Updated on 25-MAR-2003 to
XX correct PN field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
XX on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
XX standardise OS field)
XX SQ Sequence 24 AA;
Query Match 100.0%; Score 122; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNTKSIIRIQPGRAFTVIGKIG 24
DB 1 NNTKSIIRIQPGRAFTVIGKIG 24
RESULT 4
AAR29233
ID AAR29233 standard; peptide; 24 AA.
XX
AC AAR29233;
XX
DT 25-MAR-2003 (revised)
DT 14-APR-1993 (first entry)
XX
DE Heteroconjugate antibody immunogen RP135 (IIIB).
XX
XX V3 loop; gp41; envelope protein; MN; prototype; virus; variant; HIV;
XX homology; heteroconjugate; enzyme; epitope mapping; replication;
XX conjugate; immunogenic carrier; keyhole limpet hemocyanin; KLH;
XX ovalbumin; succinyl maleimidomethyl cyclohexanecarboxylate; SMCC.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 24
XX /note= "Not in the natural sequence of this isolate"
XX
XX WO9220373-A1.
XX
XX 26-NOV-1992.
XX
XX 29-APR-1992; 92WO-US003616.
XX
XX 14-MAY-1991; 91US-00699773.
XX
XX (REPK) REPLIGEN CORP.
XX
XX Higgins PJ, Potts BJ;
XX
XX WPI; 1992-415475/50.
XX
XX Hetero-conjugate antibodies for treating HIV infections - comprise an
XX antibody specific for an effector cell surface antigen and an antibody to
XX a V3 loop of GP-120 envelope protein of HIV.
XX
XX Disclosure; Page 19; 69pp; English.
XX
XX The sequences given in AAR29226-35 represent peptides which were used as
XX immunogens for the production of antibodies against HIV. These peptides
XX may be either unconjugated or conjugated to an immunogenic carrier, eg. a
XX keyhole limpet hemocyanin (KLH) or ovalbumin, using succinyl

ID AAR32406 standard; peptide; 24 AA.
 AC AAR32406;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-JUL-1993 (first entry)
 XX
 DE Sequence of peptide B1 which comprises AAs 308-331 from the V3 region of
 DE HIV-1 isolate IIIB.
 XX
 KW HIV-1; vaccine; dendritic core; ss.
 XX
 OS Synthetic.
 XX
 PN W09303766-A1.
 XX
 PD 04-MAR-1993.
 XX
 PF 11-AUG-1992; 92WO-US006688.
 XX
 PR 13-AUG-1991; 91US-00744281.
 XX
 PA (BEPK) REPLIGEN CORP.
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Tam JP, Profy AT;
 XX
 DR WPI; 1993-093730/11.
 XX
 XX New multiple antigen peptide(s) as HIV vaccines - include a dendritic
 PT core covalently bonded to peptide including the sequence IGPR.
 XX
 PR Example; Fig 1; 35pp; English.
 PS
 CC Nine peptides from the V3 regions of HIV-1 isolates IIIB, RF and MN were
 CC incorporated into tetraivalent multiple antigen peptide systems (MAPS)
 CC (see AAR32406-14). Parallel groups of three peptides with chain lengths
 CC spanning from 11-24 residues were synthesised in MAPS format for each
 CC isolate. ELIS assays demonstrated that antisera titers in mice were
 CC closely related to the length of the IIIB peptide used for the
 CC immunisation - the longer the stronger the response. There was no
 CC substantial antibody prodn. in mice against the other two series of
 CC peptides, RF (B4-B6), and MN (B7-B9), except for a low reactivity in the
 CC gp. immunised with B8 (MN isolate). Specificity tests of the B cell
 CC response demonstrated that the T cell epitope (AAR32415) also serves as a
 CC B cell epitope. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 122; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 RESULT 7
 AAR38165
 ID AAR38165 standard; peptide; 24 AA.
 XX
 AC AAR38165;
 XX
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 12-OCT-1993 (first entry)
 XX
 XX V3 loop peptide N24G.
 XX
 KW gp120; HIV-1; cytotoxic T-lymphocyte; CTL; T-helper; AIDS; infection.
 XX
 OS Human immunodeficiency virus 1.

XX W09310816-A1.
 XX
 PD 10-JUN-1993.
 XX
 PF 02-DEC-1992; 92WO-US010378.
 XX
 PR 02-DEC-1991; 91US-00800932.
 PR 16-SEP-1992; 92US-00945865.
 XX
 PA (RKA) UNIV TEXAS SYSTEM.
 XX
 PI Sastay JK, Arlinghaus RB, Platsoucas CD, Nehete PN;
 XX
 DR WPI; 1993-196739/24.
 XX
 PT Peptide composition for treating and preventing viral infections -
 PT comprise CTL-inducing epitope and HIV infection-inhibiting sequence or T
 PT helper cell-inducing sequence.
 XX
 PS Claim 19; Page 95; 130pp; English.
 XX
 CC HIV gp120 V3 loop-derived peptides (AAR38170-87) are successful in
 CC generating CTL responses, esp. peptide R15K (AAR38187); the T-helper cell
 CC -inducing peptide includes the sequence C19A (AAR38164); HIV infection-
 CC inhibiting peptides are given in AAR38188-206, and are esp. peptides
 CC R15K, N24G, E13V, R8K, T13Q and H13N (AAR38165-69). The peptides may also
 CC be derived from an influenza virus protein or a sendai virus protein
 CC (AAR41014-15). It was observed that peptide N24G (amino acids 308-311),
 CC with sequences derived from the V3 loop of HIV-1 IIIB, inhibits HIV-1
 CC infection of primary human T cells by 92% at 1 microg/ml (ca. 0.4-0.6
 CC microm). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG
 CC -2003 to correct OS field.)
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 122; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 RESULT 8
 AAY22581
 ID AAY22581 standard; peptide; 24 AA.
 XX
 AC AAY22581;
 XX
 DT 17-OCT-2003 (revised)
 DT 19-OCT-1999 (first entry)
 XX
 DE HIV LDL binding peptide, sequence A.
 XX
 KW HIV; LDL; low density lipoprotein; human; immune response; infection;
 KW immunodeficiency; neoplastic tissue; myalgic encephalomyelitis; ME;
 KW viral infection fatigue syndrome; tuberculosis; hepatitis; AIDS; ARC;
 KW acquired immunodeficiency syndrome; AIDS related complex;
 KW HIV-infected CD4 cell; immunosuppressive peptide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN W09938524-A2.
 XX
 PD 05-AUG-1999.
 XX
 PF 28-JAN-1999; 99WO-IB000149.
 XX
 PR 29-JAN-1998; 98US-0072980P.
 XX
 PA (PREN/) PRENDERGAST P T.

seq1.rag

Fri Jun 3 06:53:20 2005

XX PI Prendergast PT;
XX DR WPI; 1999-494040/41.
XX DR
XX PT Enhancing the immune response using a recombinant human low-density
XX PT lipoprotein receptor, useful for treating viral infections, especially
XX PT human immunodeficiency virus (HIV) infection.
XX PS Claim 7; Page 19; 24pp; English.
XX CC This sequence represents a HIV sequence that binds human low density
XX CC lipoprotein (LDL), and is designated sequence "A". The invention relates
XX CC to a method for enhancing the immune response in a patient with a
XX CC condition, selected from immunodeficiency (due to a viral, bacterial,
XX CC mycoplasma, fungal or parasitic infection, or from the growth of
XX CC neoplastic tissue), myalgic encephalomyelitis (ME), post inoculation or
XX CC viral infection fatigue syndrome, tuberculosis, or hepatitis. The method
XX CC comprises using a pharmaceutical composition, comprising a recombinant
XX CC human LDL receptor or a mimic molecule to the cysteine rich domain of LDL
XX CC receptor. The human recombinant LDL receptor forms pharmaceutical
XX CC compositions for: the treatment of acquired immunodeficiency syndrome
XX CC (AIDS) or ARC (AIDS related complex); reducing syncytium formation in HIV
XX CC -infected CD4 cells; treating blood or body fluid or organs to
XX CC neutralise/remove immunosuppressive peptides and/or viruses; or treating
XX CC hepatitis A, B or C. The pharmaceutical compositions also treat a viral
XX CC infection in a human or animal host. The human recombinant LDL receptor
XX CC is also useful for manufacturing medicaments for treating all the
XX CC conditions given above. The human recombinant LDL receptor is a highly
XX CC specific inhibitor of HIV-1 replication in vitro. (Updated on 17-02-2003
XX CC to standardise OS field)
XX SQ Sequence 24 AA;
Query Match 100.0%; Score 122; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNTKRSIRIQGPGRAFTVIGKIG 24
DB 1 NNTKRSIRIQGPGRAFTVIGKIG 24
RESULT 9
AAB15873
ID AAB15873 standard; peptide; 24 AA.
XX AC AAB15873;
XX DT 17-JAN-2001 (first entry)
XX DE Human chemokine derived peptide #25.
XX KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
XX KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
XX KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
XX KW basophil-mediated disease; myocardial infarction; acute ischaemia;
XX KW rheumatoid arthritis; contraception.
XX OS Synthetic.
XX PN WO200042071-A2.
XX PD 20-JUL-2000.
XX PF 12-JAN-2000; 2000WO-US000821.
XX PR 12-JAN-1999; 99US-00229071.
XX PR 17-MAR-1999; 99US-00271192.
XX PR 01-DEC-1999; 99US-00452406.
XX PR (NEOR-) NEORX CORP.
XX PA
XX CC

PI Grainger DJ, Tatalick LM;
XX DR WPI; 2000-499101/44.
XX DR
XX PT New peptide 3, amide and heterocyclic compounds and saccharide conjugates
XX PT used for inhibiting chemokine induced activity and for treating e.g.
XX PT stroke, vascular diseases, autoimmune diseases and tumor growth.
XX PS Disclosure; Fig 18; 387pp; English.
XX CC The present invention concerns the identification of a number of
XX CC chemokines which can be used to produce derivatives, agonists and
XX CC antagonists which are then useful in disease treatment. The chemokines
XX CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
XX CC These chemokine derivatives can be used to treat diseases such as
XX CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
XX CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
XX CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
XX CC rheumatoid arthritis, and can be used to prevent strokes and as
XX CC contraptives. The coding sequences for the chemokines can be used in
XX CC gene therapy for the same diseases, as well as in the production of
XX CC animal models.
XX SQ Sequence 24 AA;
Query Match 100.0%; Score 122; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNTKRSIRIQGPGRAFTVIGKIG 24
DB 1 NNTKRSIRIQGPGRAFTVIGKIG 24
RESULT 10
AAB68602
ID AAB68602 standard; peptide; 24 AA.
XX AC AAB68602;
XX DT 11-SEP-2003 (revised)
XX DT 25-APR-2001 (first entry)
XX DE HIV gp120 V3 loop peptide #2.
XX KW HIV gp120 V3 loop; liposome composition; HIV infection.
XX KW Human immunodeficiency virus 1.
XX OS US6180134-B1.
XX PN 30-JAN-2001.
XX PD 07-JUN-1995; 95US-00480332.
XX PF 23-MAR-1993; 93US-00035443.
XX PR 29-SEP-1994; 94US-00316436.
XX XX (SEQU-) SEQUUS PHARM INC.
XX XX Zalipsky S, Woodle MC, Martin FJ, Barenholz Y;
XX DR WPI; 2001-201897/20.
XX PT Liposome composition for use in treating septic shock comprises liposomes
XX PT having an outer surface layer of polyethylene glycol chains, and a
XX PT polypeptide or polysaccharide effector molecule.
XX PS Disclosure; Fig 13; 32pp; English.
XX CC The present invention relates to a liposome composition comprising
XX CC liposomes having an outer surface layer of polyethylene glycol chains,
XX CC each having a free distal end. A polypeptide or polysaccharide effector

CC molecule is covalently attached to a portion of the distal ends. The
 CC effector interferes with specific binding of pathogen or cell in a
 CC bloodstream to a target cell or cell matrix, and is rapidly removed by
 CC renal clearance from the bloodstream when administered in free form. The
 CC liposome composition may be used in treating a condition mediated by
 CC binding a pathogen or cell in the bloodstream, to a target cell or cell
 CC matrix. It can be used in treating septic shock, toxic shock, colonic
 CC inflammation, leukaemic cell proliferation, or HIV infection. The present
 CC sequence is a peptide of the V3 loop of HIV envelope protein gp120. This
 CC peptide may be used in the composition of the present invention. gp120
 CC binds to the CD4 receptor during HIV infection of lymphocytes. By
 CC introducing the present peptide, the CD4 receptors are blocked, thereby
 CC inhibiting HIV infection. (Updated on 11-SEP-2003 to standardise OS
 CC field)

XX Sequence 24 AA;

Query Match 100.0%; Score 122; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||

RESULT 1N

AAP90281
 ID AAP90281 standard; protein; 25 AA.

XX

AC AAP90281;

XX 09-SEP-2004 (revised)

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 22-JUN-1990 (first entry)

XX Peptide 135 of HIV env gene.

XX HIV; AIDS; env gene; HIV vaccine; ds.

XX Simian-Human immunodeficiency virus.

OS Unidentified.

XX EP306219-A.

XX 08-MAR-1989.

XX 25-AUG-1988; 88EP-00307889.

XX 27-AUG-1987; 87US-00090080.

XX (REPK) REPLIGEN CORP.

XX Rusche JR, Putney SD, Jayaherian K, Farley J, Grimalia R, Lynn D;

PI Petro J, Okeeffe T;

XX WPI; 1989-070387/10.

XX New HIV proteins and peptide(s) - used in diagnosis, prophylaxis or

PT therapy of AIDS, esp. for prepn. of vaccines against HIV infection.

XX Claim 1; Page 27; 29pp; English.

XX Protein derivative stimulates a lymphocyte proliferative response in HIV-
 CC infected humans, providing a means of diagnosis, protection and
 CC therapeutic value. (Updated on 25-MAR-2003 to correct PR field.) (Updated
 CC on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
 CC standardise OS field)

CC Revised record issued on 09-SEP-2004 : Correction to location

XX Sequence 25 AA;

XX

Query Match 100.0%; Score 122; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 2.7e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||

RESULT 12

AAR08276
 ID AAR08276 standard; protein; 25 AA.

XX

AC AAR08276;

XX 07-MAR-1991 (first entry)

XX HIV peptide fragment (IIIB isolate).

XX AIDS; ARC; conjugate immunogen; Neisseria outer membrane protein;

KW HIV major neutralisation determinant.

XX Human immunodeficiency virus.

XX EP402088-A.

XX 12-DEC-1990.

XX 05-JUN-1990; 90EP-00306082.

XX 06-JUN-1989; 89US-00362176.

PR 06-JUN-1989; 89US-00362177.

PR 06-JUN-1989; 89US-00362178.

PR 06-JUN-1989; 89US-00362179.

XX (MERI) MERCK & CO INC.

XX Emini EA, Marburg S, Scolnick EM, Larson VM;

XX WPI; 1990-370100/50.

XX Conjugate immunogen for AIDS and ARC treatment - composed of neutralising

PT determinant of HIV and Neisseria outer membrane.

XX Claim 2; Page 22; 24pp; English.

XX This peptide is derived from the HIV IIIB isolate and is cross- reactive
 CC with the HIV major neutralisation determinant (MntD). This MntD is used
 CC in a conjugate, covalently linked to the outer membrane protein (Omp)
 CC from Neisseria, as an immunogen for vaccination against AIDS. A cocktail
 CC of different MntD poly- peptides can be used. See also AAR08274-75 and
 CC AAR08277

XX Sequence 25 AA;

Query Match 100.0%; Score 122; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 2.7e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||

RESULT 13

AAR31276
 ID AAR31276 standard; peptide; 25 AA.

XX

AC AAR31276;

XX 12-FEB-1993 (first entry)

XX

seq1.rag

Fri Jun 3 06:53:20 2005

DE HIV principal determinant peptide.
KW AIDS; ARC; human immunodeficiency virus; vaccine; Neisseria;
KW meningitidis b; outer membrane protein complex; OMPC; PND135.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "bonds to the OMPC of the conjugate via this site"
XX
XX EP467700-A.
XX
XX 22-JAN-1992.
XX
XX 19-JUL-1991; 91EP-00306598.
XX
XX 19-JUL-1990; 90US-00555339.
XX 19-JUL-1990; 90US-00555966.
XX 19-JUN-1991; 91US-00715276.
XX 19-JUN-1991; 91US-00715278.
XX (MERI) MERCK & CO INC.
XX
XX Leanza WJ, Marburg S, Tolman RL, Emini EA;
XX WPI; 1992-026505/04.
XX Conjugate proteins comprising HIV peptide components - useful for
XX preparing vaccines for e.g. AIDS or for treating infections.
XX
XX Claim 12; Page 56; 63pp; English.
XX
XX The invention relates to a co-conjugate comprising an immunogenic protein
XX or protein complex having a first set of covalent linkages to low
XX molecular weight moieties which have an anionic or polyanionic character
XX at physiological pH, and a second set of covalent linkages to peptides
XX comprising HIV principal neutralizing determinants (PND's) or
XX immunologically equivalent peptides. Preferably at least one set of the
XX covalent linkages is comprised of maleimide derivatives; the
XX (poly)anionic moiety is composed of one to five residues of the anionic
XX form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
XX protein is the outer membrane protein complex (OMPC) of Neisseria
XX meningitidis b; and the PND peptide has a linear structure, a disulphide-
XX bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
XX bonded cyclic structure. The present sequence (PND135) is an example of a
XX PND peptide component used in the co-conjugate. The co-conjugate is
XX useful for inducing anti-peptide immune response in mammals, for inducing
XX HIV-neutralizing antibodies in mammals, for formulating vaccines to
XX prevent HIV infection or disease, including AIDS, or for treating humans
XX afflicted with HIV infection or disease
XX
XX Sequence 25 AA;
XX
XX Query Match 100.0%; Score 122; DB 2; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-10;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NNTKSIIRIQGPGRAFTVIGKIG 24
XX |||||
XX Db 1 NNTKSIIRIQGPGRAFTVIGKIG 24
XX |||||
XX
XX RESULT 14
XX AAR30031
XX ID AAR30031 standard; peptide; 25 AA.
XX
XX AC AAR30031;
XX
XX 25-MAR-2003 (revised)
XX DT 28-APR-1993 (first entry)
XX
XX HIV principle neutralising determinant 135.

XX Human immunodeficiency virus; AIDS; PND; MIEP; conjugate;
KW major immune enhancing protein; vaccine; anti-HIV antibodies; immunogen;
KW passive immunisation.
XX
XX Human immunodeficiency virus.
XX
XX EP519554-A1.
XX
XX 23-DEC-1992.
XX
XX 11-JUN-1992; 92EP-00201693.
XX
XX 19-JUN-1991; 91US-00715273.
XX
XX (MERI) MERCK & CO INC.
XX
XX Emini A, Liu MA, Marburg S, Tolman RL;
XX WPI; 1992-425771/52.
XX Conjugates of HIV-1 PND peptide(s) with the MIEP of Neisseria
XX meningitidis - useful as a vaccine for treating and preventing HIV-1
XX infection, e.g. AIDS in humans.
XX
XX Claim 9; Page 59; 66pp; English.
XX
XX The peptide is HIV principle neutralising determinant (PND) 135 and is
XX used as part of a conjugate comprising the major immune enhancing protein
XX (MIEP) of Neisseria meningitidis covalently linked to the HIV PND. The
XX conjugate may be used to prepare vaccines against HIV infections, e.g.
XX AIDS, as research tools for studying PND structure- function
XX relationships, or as immunogens for use in the passive immunisation of
XX humans. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 25 AA;
XX
XX Query Match 100.0%; Score 122; DB 2; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-10;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NNTKSIIRIQGPGRAFTVIGKIG 24
XX |||||
XX Db 1 NNTKSIIRIQGPGRAFTVIGKIG 24
XX |||||
XX
XX RESULT 15
XX AAR26712
XX ID AAR26712 standard; peptide; 25 AA.
XX
XX AC AAR26712;
XX
XX 09-FEB-1993 (first entry)
XX
XX HIV-PND-polysaccharide-protein conjugate vaccine.
XX
XX Human immunodeficiency virus; principal neutralizing determinant;
KW outer membrane protein complex; OMPC; Neisseria; AIDS; PND135.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1.1
XX /note= "Joins onto polysaccharide-protein complex via
XX this site"
XX
XX EP468714-A.
XX
XX 29-JAN-1992.
XX
XX 19-JUL-1990; 90US-00555558.
XX
XX 19-JUL-1990; 90US-00555558.


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PR 19-JUL-1990; 90US-00555974.
PR 19-JUN-1991; 91US-00715275.
PR 19-JUN-1991; 91US-00715277.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Marburg S, Tolman RL, Emini EA;
XX
XX WPI; 1992-034437/05.
XX
XX HIV peptide-polyaccharide-protein conjugates - used in vaccines or to
XX produce antibodies to prevent or treat HIV infection.
XX
XX Claim 9; Page 57; 63pp; English.
XX
XX The invention relates to a conjugate of an HIV principal neutralizing
XX determinant (PND), or an immunologically equivalent peptide (PEP),
XX covalently coupled to an immunogenic protein or protein complex through
XX an anionic polyaccharide linker. Pref. the immunogenic protein is the
XX outer membrane protein complex (OMPC) of Neisseria meningitidis b and the
XX PND peptide has a linear structure, a disulphide-bonded cyclic structure,
XX an amide-bonded cyclic structure or a thioether-bonded cyclic structure.
XX The present sequence (PND135) is an example of a PND peptide component.
XX The conjugates are used for inducing HIV-neutralising antibodies or for
XX making vaccines to prevent contraction of HIV infection or disease. The
XX antibodies can be used for passively protecting against infection by HIV,
XX or for protecting against proliferation of HIV post-infection, or for
XX treating AIDS, or in diagnostic assays
XX
XX SQ Sequence 25 AA;
XX
XX Query Match 100.0%; Score 122; DB 2; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-10;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 NNRKSIRIQRGPGRAFTVIGKIG 24
XX |||||
XX Db 1 NNRKSIRIQRGPGRAFTVIGKIG 24
XX
XX Search completed: June 3, 2005, 03:17:35
XX Job time : 165 secs

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